



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 157802

TO: Celine Qian
Location: REM/2A64/2C70
Art Unit: 1636
Tuesday, July 05, 2005

Case Serial Number: 09/921143

From: Edward Hart
Location: Biotech-Chem Library
REM-1A55
Phone: 571-272-2512

edward.hart@uspto.gov

Search Notes

Examiner Qian,

Here are the results of the search you requested.

Please feel free to contact me if you have any questions.

Edward Hart

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STIC SEARCH RESULTS FEEDBACK FORM

Biotech-Chem Library

Questions about the scope or the results of the search? Contact *the searcher* or *contact*:

Mary Hale, Information Branch Supervisor
Remsen Bldg. 01 D86
571-272-2507

Voluntary Results Feedback Form

➤ I am an examiner in Workgroup: Example: 1610

➤ Relevant prior art **found**, search results used as follows:

- ☐ 102 rejection
- ☐ 103 rejection
- ☐ Cited as being of interest.
- ☐ Helped examiner better understand the invention.
- ☐ Helped examiner better understand the state of the art in their technology.

Types of relevant prior art found:

- ☐ Foreign Patent(s)
- ☐ Non-Patent Literature
(journal articles, conference proceedings, new product announcements etc.)

➤ Relevant prior art **not found**:

- ☐ Results verified the lack of relevant prior art (helped determine patentability).
- ☐ Results were not useful in determining patentability or understanding the invention.

Comments:

Drop off or send completed forms to STIC-Biotech-Chem Library Remsen Bldg.



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SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: Celine Qian Examiner #: 78710 Date: 6/28/05
 Art Unit: 1636 Phone Number: 2-0777 Serial Number: 09/921143
 Mail Box and Bldg/Room Location: 2A64 Results Format Preferred (circle): PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of invention: Vascular Endothelial Growth Factor - 2
 Inventors (please provide full names): Coleman, Timothy

Earliest Priority Filing Date: 8/3/2000

For Sequence Searches Only Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

Please search 820 ID NO:36. (both commercial and interference). Thank you.

NA 5283

me

STAFF USE ONLY

	Type of Search	Vendors and cost where applicable
Searcher: _____	NA Sequence (#) <u>/</u>	STN _____
Searcher Phone #: _____	AA Sequence (#) _____	Dialog _____
Searcher Location: _____	Structure (#) _____	Questel/Orbit _____
Date Searcher Picked Up: <u>7/1/05</u>	Bibliographic _____	Dr. Link _____
Date Completed: <u>7/5/05</u>	Litigation _____	Lexis/Nexis _____
Searcher Prep. Review Time _____	Fulltext _____	Sequence Systems <u>DI</u>
Clerical Prep. Time: _____	Patent Family _____	WWW/Internet _____
Online Time _____	Other _____	Other (specify) _____

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 3, 2005, 01:14:22 ; Search time 21907 Seconds
(without alignments)
11685.256 Million cell updates/sec

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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues
Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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1: gb_ba.*
2: gb_htg.*
3: gb_in.*
4: gb_om.*
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9: gb_pr.*
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11: gb_sts.*
12: gb_sy.*
13: gb_un.*
14: gb_vi.*

ALIGNMENTS

RESULT 1
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LOCUS CVE18316 6074 bp DNA linear SYN 02-SEP-1999
DEFINITION Cloning vector pKGM1.
ACCESSION Y18316
VERSION Y18316.1 GI:5830187
KEYWORDS bleomycin resistance; cloning vector; kanamycin resistance;
multiple cloning site; neomycin resistance.
SOURCE Cloning vector pKGM1
ORGANISM Cloning vector pKGM1
REFERENCE 1
AUTHORS Bannasch,D. and Schwab,M.
TITLE A versatile bait vector for rapid Gal4 dependent two-hybrid screens
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 6074)
AUTHORS Bannasch,D.
TITLE Direct Submission
JOURNAL Submitted (30-OCT-1998) D. Bannasch, Institutition Division of,
Cytogenetics/H0400 Deutsches, Krebsforschungszentrum (DKFZ), Im
Neuenheimer Feld 280, D-69120 Heidelberg, FRG
REMARK Revised by author 10-JUN-1999
COMMENT Related sequences U07646, U00004, L19385.
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/note="multiple cloning site"

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	2240	42.4	8349	6 AR260588	AR260588 Sequence
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C 4	2218.4	42.0	2999	12 SYNCCDBA	L38498 Cloning vec
C 5	2218.4	42.0	2999	12 SYNCCDBA	L38499 Cloning vec
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C 8	2177.4	41.2	11403	12 AY189829	AY189829 His-3 int
C 9	2088.4	39.5	3036	12 AY222815	AY222815 Cloning v
C 10	2088.4	39.5	3210	12 AY219859	AY219859 Cloning v
C 11	2088.4	39.5	5695	12 AY222822	AY222822 Shuttle v
C 12	2088.4	39.5	5869	12 AY219861	AY219861 Shuttle v
C 13	2088	39.5	5695	12 AF445080	AF445080 Cloning v
C 14	2078	39.3	3035	12 AY222814	AY222814 Cloning v
C 15	2078	39.3	3053	12 AY222811	AY222811 Cloning v
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C 18	1793.4	33.9	4800	6 AR282049	AR282049 Sequence
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ORIGIN

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Best Local Similarity 93.4%; Pred. No. 0;
Matches 2403; Conservative 0; Mismatches 26; Indels 144; Gaps 1;
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QY 5231 CGTGTTCGCGTTCTTTAGCAGCCCTTGGCGCCCTGAGTGTCTGCGGAGCGGTG 5283
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RESULT 4
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LOCUS SYNCCDBA 2999 bp DNA linear SYN 16-MAR-2000
DEFINITION Cloning vector pKil118 ccdB gene, complete cds and
kanamycin-resistance (Km^r) gene fragment.
L38498
ACCESSION L38498.1 GI:986977
KEYWORDS ccdB gene; cloning vector; kanamycin resistance.
SOURCE Cloning vector pKil118
ORGANISM other sequences; artificial sequences; vectors.
REFERENCE 1 (bases 1 to 2999)
AUTHORS Bernard,P.
TITLE New ccdB positive-selection cloning vectors with kanamycin or
chloramphenicol selectable markers
JOURNAL Gene 162 (1), 159-160 (1995)
MEDLINE 9609896
PUBMED 7557407
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Matches 2388; Conservative 0; Mismatches 26; Indels 144; Gaps 1;
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Db 1979 CTCAGTGAACGAAACATCAGTTAAGGATTTTGGTCATGAGATTATCAAAAAGGATCT 1920
Qy 3806 CGGCATGCTGCTCCCACTCTCTGAGTTCCGGGGGATGATGCGCGGATAGCCGCTGC 3865
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Qy 3866 TGGTTTCTCGATGCCGAGGATTTGCACCTCCGCTAGAACTCCGCGAGGTCTGTCAGCC 3925
Db 1905 ----- 1906
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Db 1905 -----TTGGGGTGGCGAAGAACTCCA 1984
Qy 3986 GCATGAGATCCCGCGCTGGAGGATCATCGAGCGCGTCCCGGAAACGATTCCGAAGC 4045
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Qy 4046 CCAACCTTTCATAGAAGCGCGCTGGAATCGAATCTCGTATGCGCAGGTTGGCGCTGC 4105
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RESULT 5
SYNCCDBB/c
LOCUS

DEFINITION
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Cloning vector pKIL119 ccdB gene, complete cds and
kanamycin-resistance gene (Km^r) gene fragment.

ACCESSION
L38499.1 GI:986979

VERSION
cddB gene; kanamycin resistance.

KEYWORDS
Cloning vector pKIL119

SOURCE
other sequences; artificial sequences; vectors.

ORGANISM
1 (bases 1 to 2999)

REFERENCE
Bernard, P.

AUTHORS
New ccdB positive-selection cloning vectors with kanamycin or
chloramphenicol selectable markers

TITLE
Gene 162 (1), 159-160 (1995)

JOURNAL
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MEDLINE
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PUBMED
Location/Qualifiers

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ORIGIN

Query Match 42.0%; Score 2218.4; DB 12; Length 2999;

Best Local Similarity 93.4%; Pred. No. 0;

Matches 2388; Conservative 0; Mismatches 26; Indels 144; Gaps 1;

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Db	2999	AGCTGTTTCTGTGTGAAATTTATATCCGCTACAAATTCACACACATACGAGCCGGAA	2940	Db	1919	TCACCTAGATCCTT	1906
QY	2786	GCATAAAGTGTAAGCCTGGGGTGCTTAATGAGTGAGCTAACTACATTAATTTGCGTTGC	2845	QY	3866	TGTTTTCTGTGATGCGGAGGATTTGCATTCGCGGTAGAACTCCGCGAGGTCTCCAGCC	3925
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QY	2906	AACCGCGGGGAGAGGGGTTTCGCTATTGGGGCGCTTTCCGCTTCCGCTCACTGACT	2965	QY	3986	GCATGAGATCCCGCGCTGGAGGATCATCCAGCCGCGTCCCGGAAACGATTCGAAAGC	4045
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QY	2966	CGCTGCGCTCGGTCGTTCCGCTCGCGAGCGGTATCAGCTCACTCAAAAGGCGGTAAATAC	3025	QY	4046	CCAACTTTTCATAGAAGCGCGGTGGAATCGAAATCTCGTGATGGCAGGTTGGGCGTCG	4105
Db	2759	CGCTGCGCTCGGTCGTTCCGCTCGCGAGCGGTATCAGCTCACTCAAAAGGCGGTAAATAC	2700	Db	1823	CCAACTTTTCATAGAAGCGCGGTGGAATCGAAATCTCGTGATGGCAGGTTGGGCGTCG	1764
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DEFINITION AY189826
ACCESSION AY189826
VERSION AY189826.1 GI:28435536
KEYWORDS
SOURCE his-3 integration vector pJHAM001
ORGANISM his-3 integration vector pJHAM001
REFERENCE 1 (bases 1 to 2604)
AUTHORS other sequences; artificial sequences; vectors.
TITLE Lee,D.W., Haag,J.R. and Aramayo,R.
Construction of strains for rapid homokaryon purification after
integration of constructs at the histidine-3 (his-3) locus of
Neurospora crassa
JOURNAL Curr. Genet. 43 (1), 17-23 (2003)
PUBMED 12684841
REFERENCE 2 (bases 1 to 2604)
AUTHORS Lee,D.W., Haag,J.R. and Aramayo,R.
TITLE Direct Submission
JOURNAL Submitted (03-DEC-2002) Biology, Texas A&M University, BSBW 415,
College Station, TX 77843-3258, USA
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Matches 2359; Conservative 0; Mismatches 26; Indels 146; Gaps 2;

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AUTHORS other sequences; artificial sequences; vectors.
TITLE Kirchner, O. and Tauch, A.
JOURNAL Tools for genetic engineering in the amino acid-producing bacterium
MEDLINE Corynebacterium glutamicum
PUBMED J. Biotechnol. 104 (1-3), 287-299 (2003)
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REFERENCE 2 (bases 1 to 3210)
AUTHORS Kirchner, O. and Tauch, A.
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PUBMED Submitted (15-JAN-2003) Department of Genetics, University of
TITLE Bielefeld, Universitaetsstrasse 25, Bielefeld D-33615, Germany
JOURNAL Location/Qualifiers

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AUTHORS other sequences; artificial sequences; vectors.
TITLE 1 (bases 1 to 5695)
Kirchner, O. and Tauch, A.
JOURNAL Tools for genetic engineering in the amino acid-producing bacterium
MEDLINE Corynebacterium glutamicum
PUBMED J. Biotechnol. 104 (1-3), 287-299 (2003)
REFERENCE 2 (bases 1 to 5695)
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AUTHORS	Kirchner, O. and Tauch, A.	
TITLE	Direct Submission	
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other sequences; artificial sequences; vectors.
Kirchner,O. and Tauch,A.
Tools for genetic engineering in the amino acid-producing bacterium
Corynebacterium glutamicum
J. Biotechnol. 104 (1-3), 287-299 (2003)
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2 (bases 1 to 5869)
Kirchner,O. and Tauch,A.
Direct Submission
Submitted (15-JAN-2003) Department of Genetics, University of
Bielefeld, Universitaetsstrasse 25, Bielefeld D-33615, Germany
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Tauch,A., Zheng,Z., Puhler,A. and Kalinowski,J.			
Corynebacterium striatum chloramphenicol resistance transposon			
Tn564: genetic organization and transposition in Corynebacterium			
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2 (bases 1 to 3035)			
Kirchner,O. and Tauch,A.			
Tools for genetic engineering in the amino acid-producing bacterium			
Corynebacterium glutamicum			
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Kirchner,O. and Tauch,A.			
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REFERENCE 1 (bases 1 to 3053)
AUTHORS Tauch,A., Kirchner,O., Löffler,B., Gotker,S., Puhler,A. and Kalinowski,J.
TITLE Efficient electrotransformation of *Corynebacterium diphtheriae* with a mini-replicon derived from the *Corynebacterium glutamicum* plasmid pGAI

JOURNAL Curr. Microbiol. 45 (5), 362-367 (2002)
MEDLINE 22217619
PUBMED 12232668
REFERENCE 2 (bases 1 to 3053)
AUTHORS Tauch,A., Kirchner,O., Löffler,B., Gotker,S., Puhler,A. and Kalinowski,J.
TITLE Direct Submission
JOURNAL Submitted (22-JAN-2003) Department of Genetics, University of Bielefeld, Universitaetsstrasse 25, Bielefeld D-33615, Germany
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Db 2265 GAGGTATGTAGCGGTGCTACAGAGTTCTTGAAGTGTGCGCTTAACTACAGCTTACACTAG 2206
QY 3561 AAGAACAGTATTTGGTATCTCGGCTCTGCTGAAGCCAGTTTACCTTCGGAAGAAAGAGTTGG 3620

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 3, 2005, 01:00:02 ; Search time 2542 Seconds
(without alignments)
12302.909 Million cell updates/sec

Title: US-09-921-143-36
Perfect score: 5283
Sequence: 1 aagcttgacctatgcgact.....tgagtgcttgcgcgacgctg 5283

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues
Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_16Dec04:*
1: Geneseqn1980s:*
2: Geneseqn1990s:*
3: Geneseqn2000s:*
4: Geneseqn2001as:*
5: Geneseqn2001bs:*
6: Geneseqn2002as:*
7: Geneseqn2002bs:*
8: Geneseqn2003as:*
9: Geneseqn2003bs:*
10: Geneseqn2003cs:*
11: Geneseqn2003ds:*
12: Geneseqn2004as:*
13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5283	100.0	5283	6 ABK10062	Abk10062 Expressio
2	2240	42.4	8349	3 AAL15565	Aal15565 pMON30464
3	2017.2	38.2	6136	2 AAV29673	Aav29673 Hybrid NA
4	1793.4	33.9	4800	2 AAX52020	Aax52020 Synthetic
5	1652.4	31.3	5594	2 AAV33629	Aav33629 GENSA 981
6	1634.4	30.9	4245	12 ADJ71288	Adj71288 PCR-Blunt
7	1634.4	30.9	5285	4 Aah74865	Aah74865 Nucleotid
8	1632.8	30.9	6233	13 AD875100	Ad875100 Plasmid p
9	1632.8	30.9	5285	8 ABX94355	Abx94355 Rolling c
10	1618.2	30.6	6561	2 AAV33630	Aav33630 Plasmid v
11	1603.8	30.4	2192	6 ABQ78294	Abq78294 Nucleotid
12	1603.8	30.4	3534	9 AAL62060	Aal62060 TV-GHRH p
13	1603.8	30.4	3534	9 AAL62062	Aal62062 Wild-type
14	1603.8	30.4	3534	9 AAL62059	Aal62059 TI-GHRH p
15	1603.8	30.4	3534	9 AAL62058	Aal62058 pSP-HV-GH
16	1603.8	30.4	3534	9 AAL62061	Aal62061 15/27/28-
17	1603.8	30.4	3534	9 AAL60444	Aal60444 TI-GHRH p
18	1603.8	30.4	3534	9 AAL60445	Aal60445 TV-GHRH p
19	1603.8	30.4	3534	9 AAL60446	Aal60446 15/27/28
20	1603.8	30.4	3534	9	

21	1603.8	30.4	3534	9 AAL60443	Aal60443 pSP-HV-GH
22	1603.8	30.4	3534	9 AAL60447	Aal60447 Wild-type
23	1603.8	30.4	3534	10 ACF04661	Acf04661 Wildtype
24	1603.8	30.4	3534	10 ACF04660	Acf04660 15/27/28
25	1603.8	30.4	3534	10 ACF04657	Acf04657 HV-GHRH o
26	1603.8	30.4	3534	10 ACF04659	Acf04659 TV-GHRH o
27	1603.8	30.4	3534	10 ACF04658	Acf04658 TI-GHRH o
28	1603.8	30.4	3534	12 ADF90306	Adf90306 Wild type
29	1603.8	30.4	3534	12 ADF90302	Adf90302 HV-GHRH p
30	1603.8	30.4	3534	12 ADF90304	Adf90304 TV-GHRH p
31	1603.8	30.4	3534	12 ADF90305	Adf90305 15/27/28
32	1603.8	30.4	3534	12 ADF90303	Adf90303 TI-GHRH p
33	1603.8	30.4	3534	12 ADL70452	Adl70452 Protease
34	1603.8	30.4	3534	12 ADL70453	Adl70453 Protease
35	1603.8	30.4	3534	12 ADL70454	Adl70454 Protease
36	1603.8	30.4	3534	12 ADO31099	Ado31099 Cardiac s
37	1603.8	30.4	3534	12 ADO31100	Ado31100 Cardiac s
38	1603.8	30.4	3534	12 ADO31098	Ado31098 Cardiac s
39	1603.8	30.4	3534	12 ADO31101	Ado31101 Cardiac s
40	1603.8	30.4	3534	13 ADR23409	Adr23409 Codon opt
41	1603.8	30.4	3534	13 ADR23393	Adr23393 TI-GHRH p
42	1603.8	30.4	3534	13 ADR23394	Adr23394 TV-GHRH p
43	1603.8	30.4	3534	13 ADR23395	Adr23395 15/27/28-
44	1603.8	30.4	3534	13 ADR23392	Adr23392 Plasmid p
45	1603.8	30.4	3534	13 ADR23396	Adr23396 Plasmid e

ALIGNMENTS

RESULT 1
ABK10062
ID ABK10062 standard; DNA; 5283 BP.
AC ABK10062;
XX
XX
DT 21-MAY-2002 (first entry)
XX
DE Expression vector construct pVGI.1 containing VEGF-2 insert.
XX
XX Human; vascular endothelial growth factor 2; VEGF-2; ds; pVGI.1;
KW chronic limb ischaemia; myocardial ischaemia; autoimmune disorder; pHE4a;
KW allergic reaction; organ rejection; inflammatory condition; arrhythmia;
KW hyperproliferative disorder; viral infection; bacterial infection;
KW fungal infection; parasitic infection; cardiovascular disorder; embolism;
KW heart valve disease; aneurysm; arterial occlusive disorder; gene therapy.
XX
XX Synthetic.
OS
PN WO200211769-A1.
XX
PD 14-FEB-2002.
XX
PF 03-AUG-2001; 2001WO-US024658.
PR
XX
XX 04-AUG-2000; 2000US-0223276P.
PA (HUMA-) HUMAN GENOME SCI INC.
XX
XX Coleman TA;
PI
XX
XX WPI; 2002-217153/27.
XX
XX Isolated nucleic acid having expression vector construct with vascular
PT endothelial growth factor-2 insert, useful for treating chronic limb
PT ischaemia or myocardial ischaemia, autoimmune disorders and allergic
XX conditions.
XX
XX Disclosure; Fig 31; 241pp; English.
PS
XX
XX The invention relates to an isolated nucleic acid comprising pVGI.1
CC expression vector construct containing the vascular endothelial growth
CC factor 2 (VEGF-2) insert. The nucleic acid is useful for producing a host

CC cell by transducing, transforming or transfecting a host cell with the
CC DNA and for treating a patient having chronic limb ischaemia or
CC myocardial ischaemia, or a disease or disorder selected from autoimmune
CC disorders (e.g. rheumatoid arthritis, dermatitis), allergic reactions or
CC conditions (e.g. asthma), organ rejection, inflammatory conditions (e.g.
CC Crohn's disease), hyperproliferative disorders (e.g. Gaucher's disease),
CC diseases due to viral, bacterial, fungal or parasitic infection,
CC cardiovascular disorders (e.g. cardiomyopathy), arrhythmia, heart valve
CC diseases, aneurysms, arterial occlusive disorders and embolism. This
CC sequence represents the pVGI.1 expression vector containing the VEGF-2
CC insert
XX
SQ Sequence 5283 BP; 1244 A; 1422 C; 1417 G; 1200 T; 0 U; 0 Other;

Query Match 100.0%; Score 5283; DB 6; Length 5283;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5283; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGCTTGACCTATGCGACTTCTACTTGGCAGTACATCTAGCTATTAGTCATCGCTAT 60
Db 1 AAGCTTGACCTATGCGACTTCTACTTGGCAGTACATCTAGCTATTAGTCATCGCTAT 60

Qy 61 TACCATGGTGATCGCGTTTGGCAGTACATCAATGGCGGTGGATAGCGTTTGACTCAG 120
Db 61 TACCATGGTGATCGCGTTTGGCAGTACATCAATGGCGGTGGATAGCGTTTGACTCAG 120

Qy 121 GGGATTCCAAAGTCTCCACCCCACTGACGTCAATGGGAGTTGTTTGGCACCAAAATCA 180
Db 121 GGGATTCCAAAGTCTCCACCCCACTGACGTCAATGGGAGTTGTTTGGCACCAAAATCA 180

Qy 181 ACAGACTTCCAAATGCTGAACAACTCCGCCCACTGACGCAATGGCGGTAGGCG 240
Db 181 ACAGACTTCCAAATGCTGAACAACTCCGCCCACTGACGCAATGGCGGTAGGCG 240

Qy 241 AACATGCTTATGTAACGGTGAGTTAGCAATGCCCTTATAAGGAGAGAAAGACCGTG 300
Db 241 AACATGCTTATGTAACGGTGAGTTAGCAATGCCCTTATAAGGAGAGAAAGACCGTG 300

Qy 301 CATGCCGATTTGGGAGTAAGTGGTATGATCGTGGTATGATCGTGGTATGATCGTGGT 360
Db 301 CATGCCGATTTGGGAGTAAGTGGTATGATCGTGGTATGATCGTGGTATGATCGTGGT 360

Qy 361 GCAACAGACGGGTCTAACACGGATTGGACCACTGAAATCCCGATTGCGAGATATT 420
Db 361 GCAACAGACGGGTCTAACACGGATTGGACCACTGAAATCCCGATTGCGAGATATT 420

Qy 421 GTATTTAAGTGCCAGCTCGATACAAATAACGGCAATTGACCACTTCCACACATTGGTGTG 480
Db 421 GTATTTAAGTGCCAGCTCGATACAAATAACGGCAATTGACCACTTCCACACATTGGTGTG 480

Qy 481 CACTGGGTTGGATCGATCCATCATGCACTCGCTGGGCTTCTCTGTGGCGTGTCTT 540
Db 481 CACTGGGTTGGATCGATCCATCATGCACTCGCTGGGCTTCTCTGTGGCGTGTCTT 540

Qy 541 CTGCTCGCGCTCGCTGCTCCGGGTCTCGGAGCGCGCGCGCGCGCGCGCTTC 600
Db 541 CTGCTCGCGCTCGCTGCTCCGGGTCTCGGAGCGCGCGCGCGCGCGCGCTTC 600

Qy 601 GAGTCCGGACTCGACCTCTCGAGCGGAGCCCGAGCGGGTGAGGCCACGGCTTATGCA 660
Db 601 GAGTCCGGACTCGACCTCTCGAGCGGAGCCCGAGCGGGTGAGGCCACGGCTTATGCA 660

Qy 661 AGCAAGATCTGGAGGACGATTACGGTCTGTGTCAGTGTAGATGAATCATGACTGTA 720
Db 661 AGCAAGATCTGGAGGACGATTACGGTCTGTGTCAGTGTAGATGAATCATGACTGTA 720

Qy 721 CTCTACCCGAATTTGGAAATGTACAAAGTGTACAGTGTACAGTGTAGTGGAGCTGGCAAT 780
Db 721 CTCTACCCGAATTTGGAAATGTACAAAGTGTACAGTGTACAGTGTAGTGGAGCTGGCAAT 780

Qy 781 AACAGAGAACAGGCCAACCTCAACTCAAGGACAGAGAGACTATAAAATTTGCTGCAGCA 840
Db 781 AACAGAGAACAGGCCAACCTCAACTCAAGGACAGAGAGACTATAAAATTTGCTGCAGCA 840

Qy 841 CATTATAATACAGAGATCTTGAAGTATTGATAATAGTGGAGAAAGACTCAATGCTATG 900
Db 841 CATTATAATACAGAGATCTTGAAGTATTGATAATAGTGGAGAAAGACTCAATGCTATG 900

Qy 901 CCACGGGAGTGTGTATAGATCTGGGAGGAGTTTGGAGTCCGACAAACACCTTCTTT 960
Db 901 CCACGGGAGTGTGTATAGATCTGGGAGGAGTTTGGAGTCCGACAAACACCTTCTTT 960

Qy 961 AAACCTCCATGTGTCTCCGTACAGATGTGGGGTGTCTGCAATAGTGGGGGTGCGAG 1020
Db 961 AAACCTCCATGTGTCTCCGTACAGATGTGGGGTGTCTGCAATAGTGGGGGTGCGAG 1020

Qy 1021 TGCATGAACACAGCAGCAGCTACCTCAGCAAGAGCTTATTATTGAAATATACAGTGCCTCTC 1080
Db 1021 TGCATGAACACAGCAGCAGCTACCTCAGCAAGAGCTTATTATTGAAATATACAGTGCCTCTC 1080

Qy 1081 TCTCAAGGCCCAACACCAAGTAAATCAGTTTGGCAATCAGTTTCTGCGGATGATG 1140
Db 1081 TCTCAAGGCCCAACACCAAGTAAATCAGTTTGGCAATCAGTTTCTGCGGATGATG 1140

Qy 1141 TCTAAACTGGATGTTTACAGCAAGTTCAATTCATTTATAGACGTTCCCTGCCAGCAACA 1200
Db 1141 TCTAAACTGGATGTTTACAGCAAGTTCAATTCATTTATAGACGTTCCCTGCCAGCAACA 1200

Qy 1201 CTACCAAGTGTGAGGCGGAAAGACCTGCCCAACAATCAATCAATGTGGAATATAC 1260
Db 1201 CTACCAAGTGTGAGGCGGAAAGACCTGCCCAACAATCAATCAATGTGGAATATAC 1260

Qy 1261 ATCTCAGATGCTCGCTCAGGAAGATTTATGTTTCTCGGATGCTGAGATGACTCA 1320
Db 1261 ATCTCAGATGCTCGCTCAGGAAGATTTATGTTTCTCGGATGCTGAGATGACTCA 1320

Qy 1321 ACAGATGGAATTCATGACATCTGTGGACCAACAAGAGAGCTGGATGAAGAGACCTGTCTAG 1380
Db 1321 ACAGATGGAATTCATGACATCTGTGGACCAACAAGAGAGCTGGATGAAGAGACCTGTCTAG 1380

Qy 1381 TGTGTCTGAGAGCGGGCTTCGGCTGCGAGCTGTGGACCCCAACAAGAACTAGACAGA 1440
Db 1381 TGTGTCTGAGAGCGGGCTTCGGCTGCGAGCTGTGGACCCCAACAAGAACTAGACAGA 1440

Qy 1441 AACTCATGCGCTGTGTGTAAACAAACCTTCTCCAGCAATGTGGGCGCAACCGA 1500
Db 1441 AACTCATGCGCTGTGTGTAAACAAACCTTCTCCAGCAATGTGGGCGCAACCGA 1500

Qy 1501 GAATTTGATGAAACACATGCGAGTGTATGTAAGAAACCTGCCCAAGAAATCAACCC 1560
Db 1501 GAATTTGATGAAACACATGCGAGTGTATGTAAGAAACCTGCCCAAGAAATCAACCC 1560

Qy 1561 CTAAATCTGGAAATATGCTGTGAATGTACAGAAAGTCCACAGAAATGCTTGTAAAA 1620
Db 1561 CTAAATCTGGAAATATGCTGTGAATGTACAGAAAGTCCACAGAAATGCTTGTAAAA 1620

Qy 1621 GGAAAGAGTTCACCAACCAACATGCTGTATGTAAGAAACCTGCCCAAGAAATCAACCC 1680
Db 1621 GGAAAGAGTTCACCAACCAACATGCTGTATGTAAGAAACCTGCCCAAGAAATCAACCC 1680

Qy 1681 AAGGCTTGTGAGCCAGGATTTTATATAGTGAAGAGTGTGTGTGTGTGTGTGTGTGTGT 1740
Db 1681 AAGGCTTGTGAGCCAGGATTTTATATAGTGAAGAGTGTGTGTGTGTGTGTGTGTGTGT 1740

Qy 1741 TGGAAAGACCAAAATGAGCTAATCTAGGATCCGTACCTCCCGGCTTTTGTCAAAAC 1800
Db 1741 TGGAAAGACCAAAATGAGCTAATCTAGGATCCGTACCTCCCGGCTTTTGTCAAAAC 1800

Qy 1801 AGCACCCTTGTGCTCTCACTTGTGGAGAGCTCTTACCTGTGTGTGTGTGTGTGTGTGTGT 1860
Db 1801 AGCACCCTTGTGCTCTCACTTGTGGAGAGCTCTTACCTGTGTGTGTGTGTGTGTGTGTGT 1860

Qy 1861 TCTTCTTACACCCATGTCCCGCGGAAAGTGGAGAGCCCAAGGTAAAGCTGTGTCTCT 1920
Db 1861 TCTTCTTACACCCATGTCCCGCGGAAAGTGGAGAGCCCAAGGTAAAGCTGTGTCTCT 1920

QY 1921 GAATTTCTATCCAAAGTGTCTAACTACCTCTGTTTGTCTTTTCAACCTTTGAGACCTTTGTAAT 1980
DB |||||
DB 1921 GAATTTCTATCCAAAGTGTCTAACTACCTCTGTTTGTCTTTTCAACCTTTGAGACCTTTGTAAT 1980
QY 1981 GTGCCCTAGGTGTGGAGGCTCTCAGGCTTAACAGTGGGGGACATTTCTGTGGGACGCT 2040
DB |||||
DB 1981 GTGCCCTAGGTGTGGAGGCTCTCAGGCTTAACAGTGGGGGACATTTCTGTGGGACGCT 2040
QY 2041 AGACATATGTAAACATGGTGTAGTGTCCAGGAGAGGTGAGAACTCTCTTTAAAGTCTCCTA 2100
DB |||||
DB 2041 AGACATATGTAAACATGGTGTAGTGTCCAGGAGAGGTGAGAACTCTCTTTAAAGTCTCCTA 2100
QY 2101 GGTGGTGAAGGCTGGCTAGGCCCCAGATAGGTACTTATTTGGGGACCCCATAGAGCACT 2160
DB |||||
DB 2101 GGTGGTGAAGGCTGGCTAGGCCCCAGATAGGTACTTATTTGGGGACCCCATAGAGCACT 2160
QY 2161 GCATCTGATGAGGATGTAAACAGATGTGTAGGTGTTTGGAGGCCCATATGTCCATTCAT 2220
DB |||||
DB 2161 GCATCTGATGAGGATGTAAACAGATGTGTAGGTGTTTGGAGGCCCATATGTCCATTCAT 2220
QY 2221 GACCAGTGTACTGTCTCACAGCCATGCAACCCCTTGCCCTGCTGTGCTGACTTGTAGAGGGGA 2280
DB |||||
DB 2221 GACCAGTGTACTGTCTCACAGCCATGCAACCCCTTGCCCTGCTGTGCTGACTTGTAGAGGGGA 2280
QY 2281 TAAAGTGAGAGAAAGCCCTGGGCTTAATCAGGGGGTGTCTCAGCTCCTCTTAACCTGGATTGT 2340
DB |||||
DB 2281 TAAAGTGAGAGAAAGCCCTGGGCTTAATCAGGGGGTGTCTCAGCTCCTCTTAACCTGGATTGT 2340
QY 2341 CCTATGTCTTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCT 2400
DB |||||
DB 2341 CCTATGTCTTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCT 2400
QY 2401 GCATGTGCAAACTGTGAGCTGGGTGAGGGCCCGGGGCGAGTGACCTTTACAGACCTTTGGCA 2460
DB |||||
DB 2401 GCATGTGCAAACTGTGAGCTGGGTGAGGGCCCGGGGCGAGTGACCTTTACAGACCTTTGGCA 2460
QY 2461 CTGAGGTGGCCCGGCAAGACGCGGCATCTGTGGATCAGTGTGCTGACACGATCTGTCTCT 2520
DB |||||
DB 2461 CTGAGGTGGCCCGGCAAGACGCGGCATCTGTGGATCAGTGTGCTGACACGATCTGTCTCT 2520
QY 2521 CTCTACCACTGGAGAACTACTGCACTAGGCCCCACCACTACCTGTGTCACCCCTCTGCA 2580
DB |||||
DB 2521 CTCTACCACTGGAGAACTACTGCACTAGGCCCCACCACTACCTGTGTCACCCCTCTGCA 2580
QY 2581 ATGAATAAAACCTTTGAAAGAGCACTACAAAGTGTGTGTACATGCGTGCATGTGCATATG 2640
DB |||||
DB 2581 ATGAATAAAACCTTTGAAAGAGCACTACAAAGTGTGTGTACATGCGTGCATGTGCATATG 2640
QY 2641 TGTGTGGGGGGAAACATGATGGGGCTGTGAGTGGTTCGGGCTTAAATCTATCTGGCA 2700
DB |||||
DB 2641 TGTGTGGGGGGAAACATGATGGGGCTGTGAGTGGTTCGGGCTTAAATCTATCTGGCA 2700
QY 2701 GCTGTCTAGACGTAAATCATGGTCTATAGCTGTCTGTGTGTGAAATGTTATCTCGCTCACA 2760
DB |||||
DB 2701 GCTGTCTAGACGTAAATCATGGTCTATAGCTGTCTGTGTGTGAAATGTTATCTCGCTCACA 2760
QY 2761 ATTCCACACAACTATGAGTGGGGCTGTGAGTGGTTCGGGCTTAAATCTATCTGGCA 2820
DB |||||
DB 2761 ATTCCACACAACTATGAGTGGGGCTGTGAGTGGTTCGGGCTTAAATCTATCTGGCA 2820
QY 2821 AGCTAACTCATAATTAATGCTGTGCTCACTGCCGCTTTTCCAGTGGGAAACCTGTGCG 2880
DB |||||
DB 2821 AGCTAACTCATAATTAATGCTGTGCTCACTGCCGCTTTTCCAGTGGGAAACCTGTGCG 2880
QY 2881 TGGCAGCTGATTAATGAATTCGGCAACGCGCGGGGAGAGCGGTTTGGGTATTTGGGGCG 2940
DB |||||
DB 2881 TGGCAGCTGATTAATGAATTCGGCAACGCGCGGGGAGAGCGGTTTGGGTATTTGGGGCG 2940
QY 2941 TCTTCCGCTTCTCGCTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3000
DB |||||
DB 2941 TCTTCCGCTTCTCGCTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3000
QY 3001 TCAGCTCACTCAAAAGGCGTAAATACGGTTTATCCACAGAAATCAGGGGATACCGAGGAAAG 3060

DB |||||
QY 3001 TCAGCTCACTCAAAAGGCGTAAATACGGTTTATCCACAGAAATCAGGGGATACCGAGGAAAG 3060
QY 3061 AACATGTGAGCAAAAGCGCAGCAAAAGCGCAGCAAAAGCGTAAAGAGGCGGTTGCTGGCG 3120
DB |||||
DB 3061 AACATGTGAGCAAAAGCGCAGCAAAAGCGCAGCAAAAGCGTAAAGAGGCGGTTGCTGGCG 3120
QY 3121 TTTTTCATAGGCTCGGCCCCCTCGAGCAGCATCACAAAATCGACCTCAAGTCAAGG 3180
DB |||||
DB 3121 TTTTTCATAGGCTCGGCCCCCTCGAGCAGCATCACAAAATCGACCTCAAGTCAAGG 3180
QY 3181 TGGCGAAAACCCGACAGCACTATAAAGATACAGGCGTTTCCCTCTGAAAGCTCCTCGTG 3240
DB |||||
DB 3181 TGGCGAAAACCCGACAGCACTATAAAGATACAGGCGTTTCCCTCTGAAAGCTCCTCGTG 3240
QY 3241 CGCTCTCTGTTCCGACCCCTGCGCTTACCGGATACCTGTCCGCTTCTCCCTTCGGGA 3300
DB |||||
DB 3241 CGCTCTCTGTTCCGACCCCTGCGCTTACCGGATACCTGTCCGCTTCTCCCTTCGGGA 3300
QY 3301 AGCGTGGCGCTTCTCATAGCTCAAGCTGTAGGTATCTCAGTTCCGTTAGGTGCTTCGC 3360
DB |||||
DB 3301 AGCGTGGCGCTTCTCATAGCTCAAGCTGTAGGTATCTCAGTTCCGTTAGGTGCTTCGC 3360
QY 3361 TCCAAAGTGGCTGTGTGCAAGAACCCCGCTTACGCGGACCGCTTATCCGTT 3420
DB |||||
DB 3361 TCCAAAGTGGCTGTGTGCAAGAACCCCGCTTACGCGGACCGCTTATCCGTT 3420
QY 3421 AACTATCTGTTGAGTCCCAACCGGTAAAGACAGCTTATCGGCACCTGGCAGCAGCACT 3480
DB |||||
DB 3421 AACTATCTGTTGAGTCCCAACCGGTAAAGACAGCTTATCGGCACCTGGCAGCAGCACT 3480
QY 3481 GGTAAACAGGATTAGCAGAGCAGGTATGTAGGCGGTGTACAGAGTTCTTGAAGTGGTGG 3540
DB |||||
DB 3481 GGTAAACAGGATTAGCAGAGCAGGTATGTAGGCGGTGTACAGAGTTCTTGAAGTGGTGG 3540
QY 3541 CCTAACTACGGCTACACTAGAGAAACAGTATTTGGTATCTGCGCTCTGTCTGAGGCGAGTT 3600
DB |||||
DB 3541 CCTAACTACGGCTACACTAGAGAAACAGTATTTGGTATCTGCGCTCTGTCTGAGGCGAGTT 3600
QY 3601 ACCTTCGGAAGAGTGTGTAGTCTTGTATCGGCAAAACCAACCCCGCTGTGAGCGT 3660
DB |||||
DB 3601 ACCTTCGGAAGAGTGTGTAGTCTTGTATCGGCAAAACCAACCCCGCTGTGAGCGT 3660
QY 3661 GGTTTTTTTTGTGCAAGCAGCAGATTTAGCGCAGAAAAAAGAGTCTCAAGAGATCCT 3720
DB |||||
DB 3661 GGTTTTTTTTGTGCAAGCAGCAGATTTAGCGCAGAAAAAAGAGTCTCAAGAGATCCT 3720
QY 3721 TTGATCTTTTCTACGGGGTCTGACGCTCAGTGGAAACGAAACTCAAGTTAAGGGATTTTG 3780
DB |||||
DB 3721 TTGATCTTTTCTACGGGGTCTGACGCTCAGTGGAAACGAAACTCAAGTTAAGGGATTTTG 3780
QY 3781 GTCATGAGATTTATCGTCGCAAAAGCGGCATCTGCTCCCTCCACTCTGTCAGTTCCGGG 3840
DB |||||
DB 3781 GTCATGAGATTTATCGTCGCAAAAGCGGCATCTGCTCCCTCCACTCTGTCAGTTCCGGG 3840
QY 3841 GCATGATCGCGGATAGCGCTGTGCTGTTTCTGATGCGCAGCAGATTTGCACTGCCGG 3900
DB |||||
DB 3841 GCATGATCGCGGATAGCGCTGTGCTGTTTCTGATGCGCAGCAGATTTGCACTGCCGG 3900
QY 3901 TAGAACTCCGCGAGGTCGTCCAGCCTCAGGCGAGCTGAAACCACTCGCGAGGGGATCG 3960
DB |||||
DB 3901 TAGAACTCCGCGAGGTCGTCCAGCCTCAGGCGAGCTGAAACCACTCGCGAGGGGATCG 3960
QY 3961 AGCGCGGGTGGCGGAGAACTCCAGCATGAGATCCCGGCTGGAGGATCATCCAGCGG 4020
DB |||||
DB 3961 AGCGCGGGTGGCGGAGAACTCCAGCATGAGATCCCGGCTGGAGGATCATCCAGCGG 4020
QY 4021 GGTTCGCCGAAACAGATTCCGAAAGCCCACTTTTATAGAGCGCGCGTGGAAATCGAAA 4080
DB |||||
DB 4021 GGTTCGCCGAAACAGATTCCGAAAGCCCACTTTTATAGAGCGCGCGTGGAAATCGAAA 4080
QY 4081 TCTCGTGTAGGCGAGGTGGGCGTGGCTTGTGCTTCAAGACCCCAAGTCCCGCTC 4140
DB |||||

Db 4081 TCTCGTGATGGCAGGTTGGCGTCGCTTGCTCGGTCAATTTGGAACCCACAGAGTCCCGCTC 4140
QY 4141 AGAAGAACTCGTCAAGAGCGGATAGAGCGGATGCGCTGCGAATCGGGAGCGCGGATAC 4200
Db 4141 AGAAGAACTCGTCAAGAGCGGATAGAGCGGATGCGCTGCGAATCGGGAGCGCGGATAC 4200
QY 4201 CGTAAAGACGAGAGCGGTGAGCCCATTTCCGCGCAAGCTCTTCAGCAATATACGGG 4260
Db 4201 CGTAAAGACGAGAGCGGTGAGCCCATTTCCGCGCAAGCTCTTCAGCAATATACGGG 4260
QY 4261 TAGCCAAACGCTATGTCTCTGATAGCGGTGCGCCACACCCAGCGGCCACAGTCGATGAATC 4320
Db 4261 TAGCCAAACGCTATGTCTCTGATAGCGGTGCGCCACACCCAGCGGCCACAGTCGATGAATC 4320
QY 4321 CAGAAAAGCGGCCATTTTCACCATGATATTCGGCAAGCAGGATCGCCATGGGTACGA 4380
Db 4321 CAGAAAAGCGGCCATTTTCACCATGATATTCGGCAAGCAGGATCGCCATGGGTACGA 4380
QY 4381 CGAGATCCTCGCGTGGGCATCGCGCTTGAGCCTTGCGAACAGTTGCGCTGGCGCGA 4440
Db 4381 CGAGATCCTCGCGTGGGCATCGCGCTTGAGCCTTGCGAACAGTTGCGCTGGCGCGA 4440
QY 4441 GCCCCTGATGCTCTTCGTCAGATCATCTCTGATCGAAGACCGGTTCCATCCGAGTAC 4500
Db 4441 GCCCCTGATGCTCTTCGTCAGATCATCTCTGATCGAAGACCGGTTCCATCCGAGTAC 4500
QY 4501 GTGCTGCTCGATGCGATGTTTCGCTTGCTGCGAATGGGONAGGTAGCGGATCAAGCG 4560
Db 4501 GTGCTGCTCGATGCGATGTTTCGCTTGCTGCGAATGGGONAGGTAGCGGATCAAGCG 4560
QY 4561 TATGACAGCGCCGATTTGCATCAGCCATGATGATGATCTTCTCGGAGGAGCAAGGTAG 4620
Db 4561 TATGACAGCGCCGATTTGCATCAGCCATGATGATGATCTTCTCGGAGGAGCAAGGTAG 4620
QY 4621 ATGACAGGAGATCCTGCCCCGCACTTCGCCCAATAGCAGCCAGTCCCTTCCCGCTTCAG 4680
Db 4621 ATGACAGGAGATCCTGCCCCGCACTTCGCCCAATAGCAGCCAGTCCCTTCCCGCTTCAG 4680
QY 4681 TGACAAAGTGCAGACAGCTGCGCAAGGAACGCCGCTGCGCCAGCCAGATAGCCGG 4740
Db 4681 TGACAAAGTGCAGACAGCTGCGCAAGGAACGCCGCTGCGCCAGCCAGATAGCCGG 4740
QY 4741 CTCCTCTGCTCGCTGATTCATTCAGGGCACCGGACAGGTGCGTTCGACAAAAGAACCG 4800
Db 4741 CTCCTCTGCTCGCTGATTCATTCAGGGCACCGGACAGGTGCGTTCGACAAAAGAACCG 4800
QY 4801 GCGCCCCCTGCGCTGACAGCGGAACACGCGCGCATCAGACGACCGGATTTGTGTTGTG 4860
Db 4801 GCGCCCCCTGCGCTGACAGCGGAACACGCGCGCATCAGACGACCGGATTTGTGTTGTG 4860
QY 4861 CCCAGTCATAGCCGAATAGCTCTCCACCAAGCGCGCGAGAACCTGGGTGCAATCCAT 4920
Db 4861 CCCAGTCATAGCCGAATAGCTCTCCACCAAGCGCGCGAGAACCTGGGTGCAATCCAT 4920
QY 4921 CTGTGTTCAATCATCGCAAGCATCTCTCATCTCTCTGATCAGATCTTGATCCCTCG 4980
Db 4921 CTGTGTTCAATCATCGCAAGCATCTCTCATCTCTCTGATCAGATCTTGATCCCTCG 4980
QY 4981 GCCATCAGATCTCTGGCGGCAAGAACCCATCCAGTTTACTTTTGCAAGGGCTTCCCAACT 5040
Db 4981 GCCATCAGATCTCTGGCGGCAAGAACCCATCCAGTTTACTTTTGCAAGGGCTTCCCAACT 5040
QY 5041 TACCAGAGGCGGCCAGTGGCAATTCGGTTGCTTGTGTCATATAAACCGCCAGT 5100
Db 5041 TACCAGAGGCGGCCAGTGGCAATTCGGTTGCTTGTGTCATATAAACCGCCAGT 5100
QY 5101 CTAGCTATGCCATGTAAAGCCCACTGCAAGTACCTGCTTTCTTTTGGCTTGGCTTTT 5160
Db 5101 CTAGCTATGCCATGTAAAGCCCACTGCAAGTACCTGCTTTCTTTTGGCTTGGCTTTT 5160
QY 5161 CCCTTGTCCAGATAGCCCACTGATGATGATTCATCCGGGTGTCAGCACCGTTTCTGCGGAC 5220
Db 5161 CCCTTGTCCAGATAGCCCACTGATGATGATTCATCCGGGTGTCAGCACCGTTTCTGCGGAC 5220

QY 5221 TGGCTTTCTACGTTTCGCTTCCTTTAGCAGCCCTTGGCCCTGAGTCTTGGCGCAGC 5280
Db 5221 TGGCTTTCTACGTTTCGCTTCCTTTAGCAGCCCTTGGCCCTGAGTCTTGGCGCAGC 5280
QY 5281 GTG 5283
Db 5281 GTG 5283
RESULT 2
AA15565
ID AAA15565 standard; DNA; 8349 BP.
XX
AC AAA15565;
XX
DT 28-JUL-2000 (first entry)
XX
pMON30464 plasmid.
XX
Transgenic plant; insect resistance; cry2Aa delta-endotoxin; Coleopteran;
Lepidopteran; Dipteran; plasmid transit peptide; zmsu PTP; insecticidal;
KW plasmid targeting peptide; pMON30464 plasmid; expression vector; ds.
XX
OS Synthetic.
XX
PN WO200026371-A1.
XX
PD 11-MAY-2000.
XX
PF 04-NOV-1999; 99WO-US026086.
XX
PR 04-NOV-1998; 98US-00186002.
XX
(MONS) MONSANTO CO.
XX
Corbin DR, Romano CP;
XX
WPI; 2000-376130/32.
XX
New method of expressing insecticidal proteins in plants transformed with
a Bacillus thuringiensis delta-endotoxin encoding gene resulting in
effective control of susceptible target pests.
XX
Example 1; Page 96-99; 104pp; English.
XX
Bacillus thuringiensis produce delta-endotoxins during sporulation. These
proteins are toxic to certain insects e.g. Lepidopteran and Coleopteran
larvae. An insect-resistant transgenic plant has been constructed which
contains the delta-endotoxin cry2Ab gene. The present sequence would be
used to transfer delta-endotoxin genes into plant cells and for
subsequent high expression of the cry2Ab gene. Protection may be attained
against insects such as Ostrina spp., Diatraea spp., Helicoverpa spp.,
and Spodoptera spp., in Zea mays; Heliothis virescens, Helicoverpa spp.,
Pectinophora spp., in Gossypium hirsutum; Anticarsia spp., Pseudoplusia
spp., Epinotia spp., in Glycine max; and Scirpophaga incertulas in Oryza
sativa. Expression of the endotoxin by a plant cell produces a fusion
protein comprising an amino-terminal plasmid transit peptide (zmsu PTP)
covalently linked to the delta-endotoxin. The fusion protein functions to
localise the delta-endotoxin to a subcellular organelle or compartment
XX
Sequence 8349 BP; 1959 A; 2355 C; 2088 G; 1947 T; 0 U; 0 Other;
Query Match 42.4%; Score 2240; DB 3; Length 8349;
Best Local Similarity 93.4%; Pred. No. 0;
Matches 2409; Conservative 0; Mismatches 25; Indels 144; Gaps 1;
QY 2706 CTAGACGTAATCATGTCATAGCTTTCCTGTCGTAATTCCTCCGCTCACAAATCC 2765
Db 5911 CTTGGCGTAATCATGTCATAGCTTTCCTGTCGTAATTCCTCCGCTCACAAATCC 5970
QY 2766 ACACAACATACGAGCGGAAGCATAAAGTGTAAAGCTGGGCTGCTTAATGAGTGAGCTA 2825

QY 4986 CAGATCCTTGGCGGCAAGAACCATCCAGTTTACTTTTCAGGGCTTCCCACTTACCA 5045
|||||
Db 8047 CAGATCCTTGGCGGCAAGAACCATCCAGTTTACTTTTCAGGGCTTCCCACTTACCA 8106
|||||
QY 5046 GAGGGGCCCCAGCTGGCAATTCGGGTTCGCTGTGCTGTCCATAAAACCGCCAGTCTAGC 5105
|||||
Db 8107 GAGGGGCCCCAGCTGGCAATTCGGGTTCGCTGTGCTGTCCATAAAACCGCCAGTCTAGC 8166
|||||
QY 5106 TATCGCATGTAAAGCCACCTGCAAGCTACTGCTTTCTTTCTTTCGCGTTGCGTTTCCCTT 5165
|||||
Db 8167 TATCGCATGTAAAGCCACCTGCAAGCTACTGCTTTCTTTTCGCGTTGCGTTTCCCTT 8226
|||||
QY 5166 GTCCAGATAGCCAGTAGCTGACATTCATCCGGGGTTCAGCACCGTTTCTGCGGACTGGCT 5225
|||||
Db 8227 GTCCAGATAGCCAGTAGCTGACATTCATCCGGGGTTCAGCACCGTTTCTGCGGACTGGCT 8286
|||||
QY 5226 TTCTAGCTGTTCGGCTTCCCTTTAGCAGCCCTTCGGCCCTGAGTGTTCGGGAGCGGTG 5283
|||||
Db 8287 TTCTAGCTGTTCGGCTTCCCTTTAGCAGCCCTTCGGCCCTGAGTGTTCGGGAGCGGTG 8344
|||||

RESULT 3

AAV29673/c

ID AAV29673 standard; cDNA; 6136 BP.

XX AC AAV29673;

XX AC AAV29673;

XX DT 01-SBP-1998 (first entry)

XX DE Hybrid NAMK.6 (termamyl-linker-CBDEGV) nucleotide sequence.

XX KW Starch; liquefaction; sweetener; enzyme hybrid; endoglucanase; enzyme;

XX KW cellulose binding domain; CBD; starch processing; alpha-amylase;

XX KW saccharification; Termamyl-linker-CBD fusion; ss.

XX OS Bacillus sp.

XX OS Humicola insolens.

XX PN WO9816633-A1.

XX PD 23-APR-1998.

XX PF 13-OCT-1997; 97WO-DK000448.

XX PR 11-OCT-1996; 96DK-00001130.

XX PA (NOVO) NOVO-NORDISK AS.

XX PI Bjornvad M, Pedersen S, Schulein M, Bisgardfrantzen H;

XX DR WPI; 1998-251283/22.

XX LI Liquefaction of starch for, e.g. production of sweeteners - comprises use

XX PT of enzyme hybrids including cellulose binding domain for starch.

XX PS Example 8; Page 65-67; 83pp; English.

XX CC This is the nucleotide sequence of the termamyl-linker-CBDEGV fusion

XX CC construct pNAMK6.1. This is an enzyme hybrid which can be used for the

XX CC liquefaction of starch. The enzyme hybrids contain amino acid sequences

XX CC of alpha-amylase linked to a cellulose binding domain (CBD). The CBD is

XX CC selected from the Bacillus or Humicola insolens endoglucanase, C. xylanase A

XX CC or the Humicola insolens EGV sequence. The starch is liquefied by

XX CC treating, in aqueous medium, with such an enzyme hybrid. A recombinant

XX CC expression vector comprising a construct containing isolated DNA encoding

XX CC enzyme hybrids with amylolytic activity, promoter and stop signals can be

XX CC used to transform host cells for the production of the recombinant enzyme

XX CC hybrids. The enzyme hybrids are useful in industrial starch processing

XX CC especially for the production of sweeteners. Hybrid enzymes have altered

XX CC affinity for substrate and increased activity, resulting in at least 1 of

XX CC reduced calcium ion dependence, reduced formation of Maillard reaction

XX CC products and reduced effect of alpha-amylase on subsequent

XX CC saccharification

XX SQ Sequence 6136 BP; 1475 A; 1545 C; 1712 G; 1404 T; 0 U; 0 Other;
Query Match 38.2%; Score 2017.2; DB 2; Length 6136;
Best Local Similarity 91.8%; Pred. No. 5.1e-297;
Matches 2203; Conservative 0; Mismatches 53; Indels 144; Gaps 1;
QY 2884 CAGCTGCATTAAATGAATCGGCCAAACGCGCGGGGAGAGGGGTTTCGCTATTTCGGGCGCTCT 2943
|||||
Db 4381 CATATCGCGTGTGAATAACCGCACAGATCGCGTAAGAGAGAAATACCGATCAGGCGCTCT 4322
|||||
QY 2944 TCCGGCTTCTCGCTCACTGACTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCT 3003
|||||
Db 4321 TCCGGCTTCTCGCTCACTGACTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCT 4262
|||||
QY 3004 GCTCACTCAAAGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGACAGAAAGAAC 3063
|||||
Db 4261 GCTCACTCAAAGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGACAGAAAGAAC 4202
|||||
QY 3064 ATGTGAGCAAAAGGCGCAGCAAAAGGCGCAGGAAACCGTAAAGGCGCGCTTGTCTGGCGTTT 3123
|||||
Db 4201 ATGTGAGCAAAAGGCGCAGCAAAAGGCGCAGGAAACCGTAAAGGCGCGCTTGTCTGGCGTTT 4142
|||||
QY 3124 TTCCATAGGCTCCGCCCCCTGACGAGCATCAAAAAATCGACGCTCAAGTCAGAGGTGG 3183
|||||
Db 4141 TTCCATAGGCTCCGCCCCCTGACGAGCATCAAAAAATCGACGCTCAAGTCAGAGGTGG 4082
|||||
QY 3184 CGAAACCCGACAGGACTATAAAGATACCAAGGCGTTTCCCGCTGGAGCTCCCTCGCTGCGC 3243
|||||
Db 4081 CGAAACCCGACAGGACTATAAAGATACCAAGGCGTTTCCCGCTGGAGCTCCCTCGCTGCGC 4022
|||||
QY 3244 TCTCTGTTCCGACCCCTGCTTACCGGATACCTGTCCGCTTCTCCCTTCGGGAAGC 3303
|||||
Db 4021 TCTCTGTTCCGACCCCTGCTTACCGGATACCTGTCCGCTTCTCCCTTCGGGAAGC 3962
|||||
QY 3304 GTGGCGCTTCTCATAGCTCAGCTGTAGGTATCTCAGTTCCGCTGTAGTCCGTTCGCTCC 3363
|||||
Db 3961 GTGGCGCTTCTCATAGCTCAGCTGTAGGTATCTCAGTTCCGCTGTAGTCCGTTCGCTCC 3902
|||||
QY 3364 AAGCTGGGCTGTGTGCAGAACCCCGCTTCAGCGCGACCGCTGCGCTTATCCGGTAAC 3423
|||||
Db 3901 AAGCTGGGCTGTGTGCAGAACCCCGCTTCAGCGCGACCGCTGCGCTTATCCGGTAAC 3842
|||||
QY 3424 TATCGTCTTGTAGTCCAAACCGGTAAAGACGACTTATCGCCACTGGCAGCAGCACTGGT 3483
|||||
Db 3841 TATCGTCTTGTAGTCCAAACCGGTAAAGACGACTTATCGCCACTGGCAGCAGCACTGGT 3782
|||||
QY 3484 AACAGGATTAGCAGAGCGAGGTATGTAGCGGTGTGTACAGAGTCTTGAAGTGGTGGCT 3543
|||||
Db 3781 AACAGGATTAGCAGAGCGAGGTATGTAGCGGTGTGTACAGAGTCTTGAAGTGGTGGCT 3722
|||||
QY 3544 AACTACGGCTACACTAGAAAGAACAGTATTTGGTATCTCGCTCTCTGCTGAAGCAGTTACC 3603
|||||
Db 3721 AACTACGGCTACACTAGAAAGAACAGTATTTGGTATCTCGCTCTCTGCTGAAGCAGTTACC 3662
|||||
QY 3604 TTCGAAAAAGAGTTGGTAGCTCTTGTATCCGGCAAAACCAACCCCGCTGGTAGCGGTGGT 3663
|||||
Db 3661 TTCGAAAAAGAGTTGGTAGCTCTTGTATCCGGCAAAACCAACCCCGCTGGTAGCGGTGGT 3602
|||||
QY 3664 TTTTGTGTTTGAAGCAGCAGATTAACGCGAGAAAAAAGGATCTCAAGAGATCTCTTTG 3723
|||||
Db 3601 TTTTGTGTTTGAAGCAGCAGATTAACGCGAGAAAAAAGGATCTCAAGAGATCTCTTTG 3542
|||||
QY 3724 ATCTTTTCTACCGGGTCTGACCGCTCAGTGGAAACGAAAACTACGTTTAAGGATTTTGGTC 3783
|||||
Db 3541 ATCTTTTCTACCGGGTCTGACCGCTCAGTGGAAACGAAAACTACGTTTAAGGATTTTGGTC 3482
|||||
QY 3784 ATGAGATTATCTGACCAAAAGCGGCTATCGTCCCTCCCACTCTCTGCAAGTTCGGGGGCA 3843
|||||
Db 3481 ATGAGATTATCAAAAAGGATCTTACCTAGATCCCTT----- 3446
|||||
QY 3844 TGGATGCGGGATAGCCGCTGCTGGTTCCTGGATGCCAGGATTTTGCACTGCCCGTAG 3903
|||||

Db 3445 ----- 3446
QY 3904 AACTCCGAGGTGTCCTCCAGCTCAGGACAGCAGTGAACCAACTCGCGAGGGGATCGAGC 3963
Db 3445 ----- 3446
QY 3964 CCGGGTGGCGGAAGAACTCCAGATGAGATCCCGCGCTGGAGGATCATCCAGCGGGC 4023
Db 3445 TTGGGGTGGCGGAAGAACTCCAGATGAGATCCCGCGCTGGAGGATCATCCAGCGGGC 3386
QY 4024 TCCCGGAAGACGATTCGGAAGCCCACTTTTCATAGAGCGCGGGTGGGAATCGAATCT 4083
Db 3385 TCCCGGAAGACGATTCGGAAGCCCACTTTTCATAGAGCGCGGGTGGGAATCGAATCT 3326
QY 4084 CGTGATGGCAGGTGGGGCTGCTGCTTGGTCCGCTCATTTTCGAACCCCAAGATCCCGCTCAGA 4143
Db 3325 CGTGATGGCAGGTGGGGCTGCTTGGTCCGCTCATTTTCGAACCCCAAGATCCCGCTCAGA 3266
QY 4144 AGAATCTGTCAGAGCGCGATAGAGCGGATGCGCTGCGAATCGGAGCGGCGATACCGT 4203
Db 3265 AGAATCTGTCAGAGCGCGATAGAGCGGATGCGCTGCGAATCGGAGCGGCGATACCGT 3206
QY 4204 AAGACGAGGAGCGGTGAGCCATTCGCGCCCAAGCTCTTCAGCAATATCAGCGGTAG 4263
Db 3205 AAGACGAGGAGCGGTGAGCCATTCGCGCCCAAGCTCTTCAGCAATATCAGCGGTAG 3146
QY 4264 CCAACGCTATGTCCTGATAGCGGTCCGCCACACACCCAGCGGCCACACAGTCGATGAATCCAG 4323
Db 3145 CCAACGCTATGTCCTGATAGCGGTCCGCCACACACCCAGCGGCCACACAGTCGATGAATCCAG 3086
QY 4324 AAAAGCGGCATTTTCCACCATGATATTCGGCAAGCAGGATCGCCATGGTCCAGCAGA 4383
Db 3085 AAAAGCGGCATTTTCCACCATGATATTCGGCAAGCAGGATCGCCATGGTCCAGCAGA 3026
QY 4384 GATCTCCGCTCGCGCATGCGGCTTGAGCTTGGCTGCGCAACAGTTGGCTGGCGCAGCC 4443
Db 3025 GATCTCCGCTCGCGCATGCGGCTTGAGCTTGGCGCAACAGTTGGCTGGCGCAGCC 2966
QY 4444 CTTGATGCTCTTCGTCAGATCATCTGATCGCAAGACCGGCTTCATCCGAGTACGTG 4503
Db 2965 CTTGATGCTCTTCGTCAGATCATCTGATCGCAAGACCGGCTTCATCCGAGTACGTG 2906
QY 4504 CTCGCTCGATGCGATGTTTCGCTTGGTGGTTCGAATGGGCGAGGTAGCGGATCAAGCGTAT 4563
Db 2905 CTCGCTCGATGCGATGTTTCGCTTGGTGGTTCGAATGGGCGAGGTAGCGGATCAAGCGTAT 2846
QY 4564 GCAGCGCGCGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4623
Db 2845 GCAGCGCGCGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2786
QY 4624 ACAGGAGATCCTGCCCGGCACCTTCGCCCAATAGCAGCGAGTCCCTTCGCGCTTCAGTGA 4683
Db 2785 ACAGGAGATCCTGCCCGGCACCTTCGCCCAATAGCAGCGAGTCCCTTCGCGCTTCAGTGA 2726
QY 4684 CAAAGTCGAGCAGCTGCGCAAGAACCGCCGTCGTGGCCAGCCACGATAGCGCGCTG 4743
Db 2725 CAAAGTCGAGCAGCTGCGCAAGAACCGCCGTCGTGGCCAGCCACGATAGCGCGCTG 2666
QY 4744 CTTGCTCTGCGATTCATTCAGGGCAGCGGACGATGCTGCTTTCGCAAAAAGAACCGGGC 4803
Db 2665 CTTGCTCTGCGATTCATTCAGGGCAGCGGACGATGCTGCTTTCGCAAAAAGAACCGGGC 2606
QY 4804 GCCCTTCGCTGACAGCGGACACGCGGCGATCAGAGCAGCGGATTCGCTGTTGCGCC 4863
Db 2605 GCCCTTCGCTGACAGCGGACACGCGGCGATCAGAGCAGCGGATTCGCTGTTGCGCC 2546
QY 4864 AGTCATAGCGGAATAGCTCTCCACCCAGCGCGGAGAACCTTCGCTGCAATCCATCTT 4923
Db 2545 AGTCATAGCGGAATAGCTCTCCACCCAGCGCGGAGAACCTTCGCTGCAATCCATCTT 2486
QY 4924 GTTCAATCATGCGAAACGATTCATCTCTGCTTTCGATCAGATCTTCGCTGCGCC 4983
Db 2485 GTTCAATCATGCGAAACGATTCATCTCTGCTTTCGATCAGATCTTCGCTGCGCC 2426

QY 4984 ATCAGATCCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTTTCAGGGCTTCCCAACCTTAC 5043
Db 2425 ATCAGATCCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTTTCAGGGCTTCCCAACCTTAC 2366
QY 5044 CAGAGGGCGCCCGAGCTGGCAATTCGGTTCGCTGTCCATAAAACCGCCAGTCTTA 5103
Db 2365 CAGAGGGCGCCCGAGCTGGCAATTCGGTTCGCTGTCCATAAAACCGCCAGTCTTA 2306
QY 5104 GCTATCGCCATGTAAGCCCACTGCAAGCTACCTGCTTCTTTTTCGCTTGGCTTTCCTCC 5163
Db 2305 GCTATCGCCATGTAAGCCCACTGCAAGCTACCTGCTTCTTTTTCGCTTGGCTTTCCTCC 2246
QY 5164 TTGTCAGATAGCCCACTGCAAGCTACCTGCTTCTTTTTCGCTTGGCTTTCCTCC 5223
Db 2245 TTGTCAGATAGCCCACTGCAAGCTACCTGCTTCTTTTTCGCTTGGCTTTCCTCC 2186
QY 5224 CTTTCTACGTTCGCTTCTTTTTCAGAGCCCTTTCGCTTGGCTTTCGCTTGGCTTTCCTCC 5283
Db 2185 CTTTCTACGTTCGCTTCTTTTTCAGAGCCCTTTCGCTTGGCTTTCGCTTGGCTTTCCTCC 2126

RESULT 4

AAx52020/c

ID AAX52020 standard; DNA; 4800 BP.

XX AAX52020;

XX AC AAX52020;

DT 18-JUN-1999 (first entry)

XX Synthetic DNA plasmid sequence synlux4.

XX DNA plasmid; lux A; lux B; Vibrio fischeri; luciferase; promoter;
KW tn9 kanamycin/neomycin phosphotransferase; DNA synthesis;
KW replication competent double-stranded polynucleotide; ss.

XX Synthetic.

XX WO9914318-A1.

XX 25-MAR-1999.

XX 16-SEP-1998; 98WO-US019312.

XX 16-SEP-1997; 97US-0059017P.

XX (TEXA) UNIV TEXAS SYSTEM.

XX Evans GA;

XX WPI; 1999-244029/20.

XX Synthesis of replication competent double-stranded polynucleotides.

XX Example 4; Fig 4A-C; 135pp; English.

XX The present sequence represents a synthetic DNA plasmid sequence,
designed using synthetic parts of known plasmids. Within the sequence are
included the sequences of lux A, lux B, the A and B components of the
Vibrio fischeri luciferase sequence, positions of pUC19 including the
origin of replication and replication stability sequences, and the
promoter and coding sequence for tn9 kanamycin/neomycin
phosphotransferase. The plasmid was synthesised from 192 50-mers (see
AAX52021-12) to demonstrate the method of the invention. The
specification describes a method for the synthesis of replication
competent double-stranded polynucleotides. The method comprises
generating a first set of oligonucleotides corresponding to the plus
strand and a second set corresponding to the minus strand and annealing.
The method can be used for preparing polynucleotides encoding sequences
involved in a biochemical pathway. In particular, they can be used to
produce polynucleotides encoding enzymes, e.g. hexokinase, phosphohexose
isomerase, phosphofructokinase-1, aldolase, triose-phosphate isomerase,
glyceraldehyde-3-phosphate dehydrogenase, phosphoglycerate kinase,

CC phosphoglycerate mutase, enolase or pyruvate kinase. They can also be
CC used for the preparation of viral particles, artificial genomes and
CC artificial genetic systems

XX
SQ Sequence 4800 BP; 1345 A; 1032 C; 1163 G; 1260 T; 0 U; 0 Other;
Query Match 33.9%; Score 1793.4; DB 2; Length 4800;
Best Local Similarity 91.8%; Pred. No. 4.4e-263;
Matches 1980; Conservative 0; Mismatches 1; Indels 176; Gaps 1;
QY 3127 CATAGGCTCGCCCCCTGACGAGCATCAAAAAATCGAGCTCAAGTCAGAGTGGCGCA 3186
DB 4800 CATAGGCTCGCCCCCTGACGAGCATCAAAAAATCGAGCTCAAGTCAGAGTGGCGCA 4741
QY 3187 AACCCGACGAGTATAAAGATACACAGGGCTTTCCCTCGGAAAGCTCCCTCGTGGCTCT 3246
DB 4740 AACCCGACGAGTATAAAGATACACAGGGCTTTCCCTCGGAAAGCTCCCTCGTGGCTCT 4681
QY 3247 CCGTTCCGACCTGCGCTTACCGGATACCTGTCCGCTTCTCCCTTCGGGAAGCGTG 3306
DB 4680 CCGTTCCGACCTGCGCTTACCGGATACCTGTCCGCTTCTCCCTTCGGGAAGCGTG 4621
QY 3307 GCCTTTCTCATAGCTCACGCTAGGTATCTCAGTTCCGCTGAGGTGCTTCGCTCCAAG 3366
DB 4620 GCCTTTCTCATAGCTCACGCTAGGTATCTCAGTTCCGCTGAGGTGCTTCGCTCCAAG 4561
QY 3367 CTGGGCTGTGCAAGAACCCCGTTAGCCCGACCGCTGAGGTGCTTCGCTGTAATCTAT 3426
DB 4560 CTGGGCTGTGCAAGAACCCCGTTAGCCCGACCGCTGAGGTGCTTCGCTGTAATCTAT 4501
QY 3427 CGTCTTGTAGTCCAAACCGGTAGACACGACTTATCCCACTGCGACGACCACTGTAAC 3486
DB 4500 CGTCTTGTAGTCCAAACCGGTAGACACGACTTATCCCACTGCGACGACCACTGTAAC 4441
QY 3487 AGGATTAGCAGACGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAAC 3546
DB 4440 AGGATTAGCAGACGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAAC 4381
QY 3547 TAGCGCTACACTAGAAAGAACAGTATTTGGTATCTGGCTCTGCTGAAGCAGTTACTTTC 3606
DB 4380 TAGCGCTACACTAGAAAGAACAGTATTTGGTATCTGGCTCTGCTGAAGCAGTTACTTTC 4321
QY 3607 GGAAGAAGAGTGTAGTCTTGCATCCGCAACAAACACCGCTGCTGAGCGGTGGTGT 3666
DB 4320 GGAAGAAGAGTGTAGTCTTGCATCCGCAACAAACACCGCTGCTGAGCGGTGGTGT 4261
QY 3667 TTTGTTTGCAGCAGAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATC 3726
DB 4260 TTTGTTTGCAGCAGAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATC 4201
QY 3727 TTTTCTACGGGGTCTGACGCTCAGTGGAAAGAAACTCAGTTAAGGGATTTTGGTCATG 3786
DB 4200 TTTTCTACGGGGTCTGACGCTCAGTGGAAAGAAACTCAGTTAAGGGATTTTGGTCAT- 4142
QY 3787 AGATTATCGTCGACCAAGCGGCATCGTGCCTCCCACTCCTCGCAGTTCCGGGGCATG 3846
DB 4141 ----- 4142
QY 3847 ATCGCGGATAGCGCTGCTGGTTCCTGTGATGCCGACGATTTTGCACTGCCCGTAGAAC 3906
DB 4141 ----- 4142
QY 3907 TCCGCGAGTGTCCAGCTTCAGGCGACGCTGAACCAACTCCGAGGGGATCGAGCCCG 3966
DB 4141 -----GCCCG 4137
QY 3967 GGGTGGCGAAGAACTCCAGCATGATCCCGCTGGAGGATCATCCAGCGGGCTCC 4026
DB 4136 GGGTGGCGAAGAACTCCAGCATGATCCCGCTGGAGGATCATCCAGCGGGCTCC 4077
QY 4027 CGGAAACGATTCGGAAGCCCAACCTTTTCATAGAAGCGCGGTGGAATCGAAATCTCGT 4086
DB 4076 CGGAAACGATTCGGAAGCCCAACCTTTTCATAGAAGCGCGGTGGAATCGAAATCTCGT 4017

QY 4087 GATGCGAGTTGGGCGTTCGCTTGGTCCGTCATTTTGAACCCCGAGAGTCCCGCTCAGAA 4146
DB 4016 GATGCGAGTTGGGCGTTCGCTTGGTCCGTCATTTTGAACCCCGAGAGTCCCGCTCAGAA 3957
QY 4147 ACTCGTCAAGAAGGCGATAGAAGGCGATGCGCTGCGAATCGGAGCGGGGATACCGTAAA 4206
DB 3956 ACTCGTCAAGAAGGCGATAGAAGGCGATGCGCTGCGAATCGGAGCGGGGATACCGTAAA 3897
QY 4207 GCACGAGGAAGCGGTGAGCCCATTTCCCGCCAAAGCTCTTTCAGCAATATCACGGGTAGCCA 4266
DB 3896 GCACGAGGAAGCGGTGAGCCCATTTCCCGCCAAAGCTCTTTCAGCAATATCACGGGTAGCCA 3837
QY 4267 AGCTTATGCTCTGATAGAGGTCGCGCACACCCAGCGGGCCACAGTCGATGAATCCAGAA 4326
DB 3836 AGCTTATGCTCTGATAGAGGTCGCGCACACCCAGCGGGCCACAGTCGATGAATCCAGAA 3777
QY 4327 AGCGGCCATTTTCCACCATGATATTTCCGCAAGCAGGATCGCCATGGGTACGAGAGAT 4386
DB 3776 AGCGGCCATTTTCCACCATGATATTTCCGCAAGCAGGATCGCCATGGGTACGAGAGAT 3717
QY 4387 CTTCCGCTCGGCGCATGCGCTTGAAGCTCGCGAAAGTTTCGGCTGGCGGAGCCCT 4446
DB 3716 CTTCCGCTCGGCGCATGCGCTTGAAGCTCGCGAAAGTTTCGGCTGGCGGAGCCCT 3657
QY 4447 GATGCTCTTCGTCGAGATCATCTGATCGAACAGCCGCTTCCATCCGAGTACGTGCTC 4506
DB 3656 GATGCTCTTCGTCGAGATCATCTGATCGAACAGCCGCTTCCATCCGAGTACGTGCTC 3597
QY 4507 GCTCGATGCGATGTTTTCGCTTGGTTCGAATGGCGAGTACCGGATCAAGCGTATGCA 4566
DB 3596 GCTCGATGCGATGTTTTCGCTTGGTTCGAATGGCGAGTACCGGATCAAGCGTATGCA 3537
QY 4567 GCCCGCGCATTCGATCAGCCATGATGGATATTTTCTCGGCAAGGCAAGGTGAGATGACA 4626
DB 3536 GCCCGCGCATTCGATCAGCCATGATGGATATTTTCTCGGCAAGGCAAGGTGAGATGACA 3477
QY 4627 GGAGATCTGCCCCCGGCACTTCCGCAATAGCAGCCGCTTCCGCTTCAGTGACAA 4686
DB 3476 GGAGATCTGCCCCCGGCACTTCCGCAATAGCAGCCGCTTCCGCTTCAGTGACAA 3417
QY 4687 CGTCAGACACAGCTGCGCAAGGAAAGCCCGTCTGTCGCCAGCCACGATAGCCGCTGCTC 4746
DB 3416 CGTCAGACACAGCTGCGCAAGGAAAGCCCGTCTGTCGCCAGCCACGATAGCCGCTGCTC 3357
QY 4747 CTTCTGCAAGTTTCAATTCAGGCGCACCGGACAGGTTCGCTTGAACAAAGAAACCGGGCGCC 4806
DB 3356 CTTCTGCAAGTTTCAATTCAGGCGCACCGGACAGGTTCGCTTGAACAAAGAAACCGGGCGCC 3297
QY 4807 CCTGCGCTGACAGCCGGAACACCGCGGATCAGAGCAGCCGATTTGCTGCTGTCGCCACT 4866
DB 3296 CCTGCGCTGACAGCCGGAACACCGCGGATCAGAGCAGCCGATTTGCTGCTGTCGCCACT 3237
QY 4867 CATAGCCGAATAGCTCTCCACCAGCGGCGCGGAACTTCGCTGCAATCCATCTTGT 4926
DB 3236 CATAGCCGAATAGCTCTCCACCAGCGGCGCGGAACTTCGCTGCAATCCATCTTGT 3177
QY 4927 CAATCATGCGAAACGATCTCATCTGCTCTTTGATCAGATCTTGAATCCCTTCGCGCATC 4986
DB 3176 CAATCATGCGAAACGATCTCATCTGCTCTTTGATCAGATCTTGAATCCCTTCGCGCATC 3117
QY 4987 AGATCTTGGCGGCAAGAACCATCCAGTTTATCTTTCAGGGCTTCCCAACCTTACCAG 5046
DB 3116 AGATCTTGGCGGCAAGAACCATCCAGTTTATCTTTCAGGGCTTCCCAACCTTACCAG 3057
QY 5047 AGGCGGCCCCAGCTGGCAATTCGGTTCGCTTGTCTGCTCAATAAAACCGCCAGCTTAGCT 5106
DB 3056 AGGCGGCCCCAGCTGGCAATTCGGTTCGCTTGTCTGCTCAATAAAACCGCCAGCTTAGCT 2997
QY 5107 ATCGGCATGTAAGCCCATGCAAGCTA CTTGCTTTCTCTTTTGGGCTTGGGTTTCCCTTG 5166
DB 2996 ATCGGCATGTAAGCCCATGCAAGCTA CTTGCTTTCTCTTTTGGGCTTGGGTTTCCCTTG 2937

QY 5167 TCAGATAGCCAGTAGCTGACATTATTCGCGGGTCAGCAACCGTTTCTCGGAGTGGCTT 5226
Db 2936 TCAGATAGCCAGTAGCTGACATTATTCGCGGGTCAGCAACCGTTTCTCGGAGTGGCTT 2877
QY 5227 TCTACGTGTTCCGCTTCTCTTTAGCAGCCCTTTCGCGCCTGAGTGTTCGCGCAGCGTG 5283
Db 2876 TCTACGTGTTCCGCTTCTCTTTAGCAGCCCTTTCGCGCCTGAGTGTTCGCGCAGCGTG 2820

RESULT 5

AAV33629/c

ID AAV33629 standard; DNA; 5594 BP.

XX AAV33629;

AC AAV33629;

XX 29-DEC-1998 (first entry)

XX GENSA 981, a monomeric DNA sequence produced by the invention.

XX Class IIS restriction endonuclease recognition site;

XX endogenous mouse promoter element; tissue-specific gene expression;

XX hormone-specific gene expression; ss;

XX developmental-specific gene expression.

XX Synthetic.

XX WO9838326-A1.

XX 03-SEP-1998.

XX 28-FEB-1998; 98WO-US003918.

XX 28-FEB-1997; 97US-0070910P.

XX (NATU-) NATURE TECHNOLOGY CORP.

XX Hodgson CP, Zink MA, Xu G;

XX WPI; 1998-495399/42.

XX Method for assembling gene or gene vector - comprises use of primers

XX containing class IIS restriction endonuclease recognition sites.

XX Example 2; Page 107-110; 141pp; English.

XX The invention provides a novel method for directing self-assembly of a

XX gene having three or more fragments in a directionally and spatially

XX ordered fashion to produce a gene or a gene vector. The method involves

XX usage of primers, containing class IIS restriction endonuclease

XX recognition sites, for isolation of these fragments. As described in the

XX disclosure, the method may also use a vector for the incorporation and

XX screening of endogenous mouse promoter elements for the identification of

XX cell specific promoters. In the example given, plasmids pBK-CMV

XX (AAV33626), pVLAMB (AAV33623) and pVIOVNH-900 (AAV33621) were used as

XX templates from which six fragments were amplified. Each of the fragments

XX contained different regulatory sequences. The six PCR fragments were

XX designed to self-assemble into a retro-vector using the method of the

XX invention. The present sequence, designated as GENSA 981, represents the

XX monomeric DNA sequence of the six ligated fragments. In general, the

XX method is claimed to be useful for isolating and identifying regulatory

XX sequences from a cell, including those for enhanced biological activity,

XX or tissue-specific, hormone-specific or developmental-specific gene

XX expression

XX Sequence 5594 BP; 1232 A; 1519 C; 1518 G; 1325 T; 0 U; 0 Other;

XX Query Match 31.3%; Score 1652.4; DB 2; Length 5594;

XX Best Local Similarity 85.4%; Pred. No. 1e-241;

XX Matches 1916; Conservative 0; Mismatches 261; Indels 67; Gaps 4;

XX

QY 3107 CGCGTGTGCGGTTTTCATAGGCTCGCCCCCTGACGAGCATCAAAAATCGAC 3166

Db 5591 CGCGTGTGCGGTTTTCATAGGCTCGCCCCCTGACGAGCATCAAAAATCGAC 5532

QY 3167 GCTCAAGTCAGAGTGGCGAAACCCGACAGGACTATAAGATACAGGCGTTTCCCGCTG 3226
Db 5531 GCTCAAGTCAGAGTGGCGAAACCCGACAGGACTATAAGATACAGGCGTTTCCCGCTG 5472
QY 3227 GAAGCTCCCTCGTGGCGCTCTCTGTTCCGACCTCGCGCTTACCGGATACCTGTCCGCT 3286
Db 5471 GAAGCTCCCTCGTGGCGCTCTCTGTTCCGACCTCGCGCTTACCGGATACCTGTCCGCT 5412
QY 3287 TTCTCCCTTCGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGTATCTCAGTTCCG 3346
Db 5411 TTCTCCCTTCGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGTATCTCAGTTCCG 5352
QY 3347 TGTAGTTCGTTCCCTCCAAAGCTGGGCTGTGTGCACGAACCCCGCTTTCAGCCCGACCGCT 3406
Db 5351 TGTAGTTCGTTCCCTCCAAAGCTGGGCTGTGTGCACGAACCCCGCTTTCAGCCCGACCGCT 5292
QY 3407 GGGCTTATCCGTTAACTATCTGTTAGTCCAAACCCCGTAAAGACACGACTTATCGCCAC 3466
Db 5291 GGGCTTATCCGTTAACTATCTGTTAGTCCAAACCCCGTAAAGACACGACTTATCGCCAC 5232
QY 3467 TGGCAGCAGCCACTGTTAAAGAGTTAGCAGAGGAGTATGTAGCGGCTGTACAGAGT 3526
Db 5231 TGGCAGCAGCCACTGTTAAAGAGTTAGCAGAGGAGTATGTAGCGGCTGTACAGAGT 5172
QY 3527 TCTTGAAGTGGTGGCTTAACCTACGGCTACACTAGAAGAACAGTATTTGGTATCTCGCTC 3586
Db 5171 TCTTGAAGTGGTGGCTTAACCTACGGCTACACTAGAAGAACAGTATTTGGTATCTCGCTC 5112
QY 3587 TGTGTAAGCCAGTTACCTTCGGAAAGAGTTGTTAGTCTTTGATCCCGCAACAAACCA 3646
Db 5111 TGTGTAAGCCAGTTACCTTCGGAAAGAGTTGTTAGTCTTTGATCCCGCAACAAACCA 5052
QY 3647 CGCTGTTAGCGGTGGTGTGTTTTCGAAGCAGCAGATTAAGCGCAGAAAAAAGGAT 3706
Db 5051 CGCTGTTAGCGGTGGTGTGTTTTCGAAGCAGCAGATTAAGCGCAGAAAAAAGGAT 4992
QY 3707 CTCAGAAGATCCTTTTGTATCTGCGGGCTCTGACGCTC-----AGTGGAAACG 3757
Db 4991 GGTGTGGGCTCTTTTATTTAGCTCGGGGAGCAGAGCGCGACAGAGGAGGAGCG 4932
QY 3758 AAAATCTACGTTAAGGATTTTGGTCAAGAGATTAATCGTCAGCAAAAGCGGCATCGTGC 3817
Db 4931 AACTGATTGGTTAGTTCAAAATAGGCACAGGCTCATTTTTCAGGCTCTTGGGCGACCCCTGGA 4872
QY 3818 CTC-----CCACTCTCGCAGTTTCGGGGGCATGATGCGCGGATAGCGCTG 3864
Db 4871 AACTCTGATGTTTCTTAGAAACTGTGAGGGCTGGACCGCATCTGGGGACCATCTGTT 4812
QY 3865 CTGGTTTCTGATGTCGACGAGGATTTGC-----ACTGCGGTAGAACTCCCGGAG 3914
Db 4811 CTGGGGCTGAGCGGGGACGAACTGCTTACCACAGATATCTGTTTGGCCCATATTCA 4752
QY 3915 GTCTCCAGCTTCAGGAGCAGAGTGAACCACTCGGAGGGGATCGAGCCGGGTTGGCG 3974
Db 4751 GCTGTTCCATCTGTTTGGCCCTGAGCGGGGACGAACTGCTTACCACAGATATCTG 4692
QY 3975 GAAGAACTCCAGATGAGATCCCGCGCTGGAGGATCATCCAGCGGCTCCCGGAAAC 4034
Db 4691 TTTGGCCCATATTTCAGCTGTTCCATCTGTTCTGACCTTGTATCTGAACTTCTTATTC 4632
QY 4035 GATTCCGAAGCCCAACCTTTTCATAGAAGCGCGGTGGAATCGAAATCTCG----- 4085
Db 4631 AGTTATGATATTTTTCATGCTTGCAGAAATGGCGTTACTTAAAGTACGTTGCAAAACCTA 4572
QY 4086 -----TGATGGCAGTTGGGCTCGCTTGGTGGTCAATT 4119
Db 4571 CAGGTGGGCTCTTTCAATTCCTCCCTTTTCTGAGGTTGGGCTCGCTTGGTGGTCAATT 4512
QY 4120 TCGAACCAGAGTCCCGCTCAGAGAACTCTGTAAGAGGCGATAGAGGCGATCGCT 4179
Db 4511 TCGAACCAGAGTCCCGCTCAGAGAACTCTGTAAGAGGCGATAGAGGCGATCGCT 4452

Db 4065 TTTTCCATAGGCTCCGCCCTCTGACGAGCATACAAAAATCGAGCTCAAGTCAGAGGT 4006
Qy 3182 GGGGAAACCCGACAGACTATAAGATACACAGGCGTTTCCCTCTGGAAGCTCCCTCGTGC 3241
Db 4005 GGGGAAACCCGACAGACTATAAGATACACAGGCGTTTCCCTCTGGAAGCTCCCTCGTGC 3946
Qy 3242 GCTCTCCTGTTCCGACCCCTCGGTTTACCGGATACCTGTGCGCTTCTCTCCCTCGGAA 3301
Db 3945 GCTCTCCTGTTCCGACCCCTCGGTTTACCGGATACCTGTGCGCTTCTCTCCCTCGGAA 3886
Qy 3302 GCGTGGCGCTTCTCATAGCTCAGCTGTAGGTATCTCAGTTCGGTGTAGGTGCTCGCT 3361
Db 3885 GCGTGGCGCTTCTCATAGCTCAGCTGTAGGTATCTCAGTTCGGTGTAGGTGCTCGCT 3826
Qy 3362 CCAAGCTGGGCTGTGTGACGAAACCCCTCGTTCAGCCCGGACCGCTGCGCTTATCCGGTA 3421
Db 3825 CCAAGCTGGGCTGTGTGACGAAACCCCTCGTTCAGCCCGGACCGCTGCGCTTATCCGGTA 3766
Qy 3422 ACTATCGCTCTGAGTCCAAACCCGGTAAGACACGACTTATCGCACTGGGACGCACTG 3481
Db 3765 ACTATCGCTCTGAGTCCAAACCCGGTAAGACACGACTTATCGCACTGGGACGCACTG 3706
Qy 3482 GTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTCTTGAAGTGTGGC 3541
Db 3705 GTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTCTTGAAGTGTGGC 3646
Qy 3542 CTAACCTACGGCTACACTAGAAAGAACAGTATTTGGTATCTCGCTCTGCTGAAGCAGTTA 3601
Db 3645 CTAACCTACGGCTACACTAGAAAGAACAGTATTTGGTATCTCGCTCTGCTGAAGCAGTTA 3586
Qy 3602 CTTTCGGAAGAGTTGTTAGTCTTTGATCCGGCAAAACAAACACCGCTGGTAGCGGTG 3661
Db 3585 CTTTCGGAAGAGTTGTTAGTCTTTGATCCGGCAAAACAAACACCGCTGGTAGCGGTG 3526
Qy 3662 GTTTTTTTGTTCCAGCAGCAGATTACGCGCAGAAAGAAAGATCTCAAGAGATCTT 3721
Db 3525 GTTTTTTTGTTGCAAGCAGCAGATTACGCGCAGAAAGAAAGATCTCAAGAGATCTT 3466
Qy 3722 TGATCTTTTCTACGGGCTCTGAGCTCAGTGGAAACGAAACTCAGCTTAAAGGATTTGG 3781
Db 3465 TGATCTTTTCTACGGGCTCTGAGCTCAGTGGAAACGAAACTCAGCTTAAAGGATTTGG 3406
Qy 3782 TCATGAGATPATC----- 3794
Db 3405 TCATGAGATPATCAAAAAGGATCTTCACCTAGATCCTTTTAAATTAATAAGATTTTA 3346
Qy 3795 -----GTCAACA 3802
Db 3345 GCACGTGTCACTCCTCTCGGCCACGAAAGTGCACGAGTTGCGCGCGGCTCGCA 3286
Qy 3803 AAGCGGCATCGTGCCTCCCACTCTCTGCAAGTTGCGGGCATGATGCGCGGATAGCCGC 3862
Db 3285 GGGCGAACTCCCGCCCTCAGCTGCTCGCCGATCTCGGTATGCGCGGCCCGGAGCGT 3226
Qy 3863 TGCTGTTTCTTGATTCGCAAGGATTTGCACTGCGGTAGAACTCCGCGAGTCTGCCA 3922
Db 3225 CCGGAAAGTTGTTGGGACACGACCTCCGACCACTCGGCTACAGCTCGTCCAGGCCGCA 3166
Qy 3923 GCC----- 3925
Db 3165 CCACACCCAGGCCAGGCTGTTGTCGGGCACCACTCTGTCCTGGACCGCGCTGATGAACA 3106
Qy 3926 ---TCAGGCAGCAGCTGAACTCGCAGAGGGATCGAGCCGGGCTGGGGAAGAACT 3982
Db 3105 GGGTCACTGCTCCCGGACACACCGCGGAAGTCTCTCCACGAAGTCCCGGGAAC 3046
Qy 3983 CCAGCATGAGATCCCGCGCTGGAGGATCATCAGCCCGGCTCCCGGAAACGATTTCCGA 4042
Db 3045 CGAGCCGCTCGGTCCAGAACTCGACCGCTCCGCGCAGCTCGCGCGGTGAGCACCGGAA 2986
Qy 4043 AGCCCAACCTTTTCATAGAGCGCGGTGGAATCGAAATCTCTGTATGGCAGGTTGGCG 4102
Db 2985 CGGCACTGGTCAACTTGGCCATGTTGGCCCTCTCTCAGCTGCTATTATTGAAGCATTTATC 2926

Qy 4103 TCGCTTGGTCCGTCAITTCGAAACCCAGAGTCCCG----- 4137
Db 2925 AGGGTTATTCTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACAAATAG 2866
Qy 4138 ----- 4137
Db 2865 GGGTTCGGGCACATTTTCCCGAAAAAGTCCACCTGTATGCGGTGTGAATATCCGCACAG 2806
Qy 4138 -----CTCAGAAAGACTC 4150
Db 2805 ATCGGTAAGAGAAAAATACCGCATCAGGAAATTTGTAAAGCGTTAATAATTTAGAAAGACTC 2746
Qy 4151 GTCAAGAGCGGATAGAGCGGATGCGCTCGCAATCGGAGCGCGGATACCGTTAAAGCAC 4210
Db 2745 GTCAAGAGCGGATAGAGCGGATGCGCTCGCAATCGGAGCGCGGATACCGTTAAAGCAC 2686
Qy 4211 GAGGAAGCGGTAGCGCCATTCGCGCCAAAGCTCTTCAGCAATATCAAGGTAGCCAAAGC 4270
Db 2685 GAGGAAGCGGTAGCGCCATTCGCGCCAAAGCTCTTCAGCAATATCAAGGTAGCCAAAGC 2626
Qy 4271 TATGTCTCTGATAGCGGTCCGCCACACCCAGCGGCCACAGTCGATGATCCAGAAAGCG 4330
Db 2625 TATGTCTCTGATAGCGGTCCGCCACACCCAGCGGCCACAGTCGATGATCCAGAAAGCG 2566
Qy 4331 GCCATTTTCCACCATGATATTCGGCAAGCAGGATCGCCATGGGTCAAGAGAGATCTCTC 4390
Db 2565 GCCATTTTCCACCATGATATTCGGCAAGCAGGATCGCCATGGGTCAAGAGAGATCTCTC 2506
Qy 4391 GCGTTCGGGATGCGCGCTTGAGCTTGCGAAACAGTTCGGTGGCGGAGCCCTGATG 4450
Db 2505 GCGTTCGGGATGCGCGCTTGAGCTTGCGAAACAGTTCGGTGGCGGAGCCCTGATG 2446
Qy 4451 CTCTTCGTCCAGATCATCTGATGCAAGACGCGCTTCATCCGAGTACGTCTCGCTC 4510
Db 2445 CTCTTCGTCCAGATCATCTGATGCAAGACGCGCTTCATCCGAGTACGTCTCGCTC 2386
Qy 4511 GATCGCATGTTTCGTTCGTTCGAAATGGGAGGTAGCGGATCAAGGTATGCAAGCGG 4570
Db 2385 GATCGCATGTTTCGTTCGTTCGAAATGGGAGGTAGCGGATCAAGGTATGCAAGCGG 2326
Qy 4571 CCGCATTTGATCAGCCATGATGATACTTTCTCGGAGAGCAAGGTGATGACAGGAG 4630
Db 2325 CCGCATTTGATCAGCCATGATGATACTTTCTCGGAGAGCAAGGTGATGACAGGAG 2566
Qy 4631 ATCTGCCCCGGCACTTCGCCCAATAGCAGCCAGTCCCTTCCGCTTTCAGTGAACAGTC 4690
Db 2265 ATCTGCCCCGGCACTTCGCCCAATAGCAGCCAGTCCCTTCCGCTTTCAGTGAACAGTC 2206
Qy 4691 GAGCAGCTGCGCAAGGAAACCGCTGCGGACGACGATAGCGCGCTGCGCTCGTC 4750
Db 2205 GAGCAGCTGCGCAAGGAAACCGCTGCGGACGACGATAGCGCGCTGCGCTCGTC 2146
Qy 4751 CTGCAAGTTCATTCAGGCAACCGGACAGGTCGTTCGTAAGAAAGAACCGGCGCCCTG 4810
Db 2145 TTGCAAGTTCATTCAGGCAACCGGACAGGTCGTTCGTAAGAAAGAACCGGCGCCCTG 2086
Qy 4811 CGCTGACGCGGAAACACCGCGGATCAGAGCGCGATTTGTTGTGCGGAGTCATA 4870
Db 2085 CGCTGACGCGGAAACACCGCGGATCAGAGCGCGATTTGTTGTGCGGAGTCATA 2026
Qy 4871 GCCGAATAGCTCTCCACCAAGCGCGGAGAACTCGGTGCAATCTTGTTCAT 4930
Db 2025 GCCGAATAGCTCTCCACCAAGCGCGGAGAACTCGGTGCAATCTTGTTCAT 1966
Qy 4931 CATGCAAAACGATCTCTATCTCTCTTTGATCAGATCTTGATCCCTCGGCAATCAGAT 4990
Db 1965 CATGCAAAACGATCTCTATCTCTCTTTGATCAGAGCTTGATCCCTCGGCAATCAGAT 1906
Qy 4991 CTTTGGCGGCAAGAAAGCCATCCAGTTTACCTTTGAGGCTTCCCACTTACAGAGGG 5050
Db 1905 CTTTGGCGGCAAGAAAGCCATCCAGTTTACCTTTGAGGCTTCCCACTTACAGAGGG 1846

Db 5285 |||||CTTCCGCTTCTCGCTCACTGACTCGCTGGCTCGGTGGTTCGGCTGCGCGAGCGGTAT 5226
Qy 3002 CAGCTCACTCAAGGCGGTAAATACGGTTATCCACAGAATCAGGGGATAACGACGAGAAAGA 3061
Db 5225 CAGCTCACTCAAGGCGGTAAATACGGTTATCCACAGAATCAGGGGATAACGACGAGAAAGA 5166
Qy 3062 ACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAAACCGTAAAAAGGCGCGGTGCTGGCGT 3121
Db 5165 ACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAAACCGTAAAAAGGCGCGGTGCTGGCGT 5106
Qy 3122 TTTTCCATAGGCTCGSCCCCTGACGAGCATCACAAAATCGACGCTCAAGTCAAGGT 3181
Db 5105 TTTTCCATAGGCTCGSCCCCTGACGAGCATCACAAAATCGACGCTCAAGTCAAGGT 5046
Qy 3182 GCGAAACCCGACAGACTATAAAGATACAGCGGTTTCCCTCGGAAGCTCCCTCGTGC 3241
Db 5045 GCGAAACCCGACAGACTATAAAGATACAGCGGTTTCCCTCGGAAGCTCCCTCGTGC 4986
Qy 3242 GCTCTCTGTTCCGACCCCTGCGCTTACCGGATACCTGTCCGCTTTTCTCCCTCGGGAA 3301
Db 4985 GCTCTCTGTTCCGACCCCTGCGCTTACCGGATACCTGTCCGCTTTTCTCCCTCGGGAA 4926
Qy 3302 GGTGGCGCTTCTCATAGCTCACGCTGAGGTATCTCAGTTTCGGGTAGGTGCTTCGCT 3361
Db 4925 GGTGGCGCTTCTCATAGCTCACGCTGAGGTATCTCAGTTTCGGGTAGGTGCTTCGCT 4866
Qy 3362 CCAAGCTGGGCTGTGTGACGAAACCCCGCTTACGCCCGCGCTGCGCTTATCCGGTA 3421
Db 4865 CCAAGCTGGGCTGTGTGACGAAACCCCGCTTACGCCCGCGCTGCGCTTATCCGGTA 4806
Qy 3422 ACTATCGTCTGAGTCCAAACCGGTTAAGACAGACTTATCGGCACTGCGCAGCAGCCACTG 3481
Db 4805 ACTATCGTCTGAGTCCAAACCGGTTAAGACAGACTTATCGGCACTGCGCAGCAGCCACTG 4746
Qy 3482 GTAACAGGATTAGCAGAGCGAGTATGTAGGCGGTGTACAGATTCTTGAAGTGTGGC 3541
Db 4745 GTAACAGGATTAGCAGAGCGAGTATGTAGGCGGTGTACAGATTCTTGAAGTGTGGC 4686
Qy 3542 CTAACCTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTA 3601
Db 4685 CTAACCTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTA 4626
Qy 3602 CCTTCGGAAAGAGTTGAGTCTTTGATTCGGGCAAAACCAACCGCTGTGTAGCGGTG 3661
Db 4625 CCTTCGGAAAGAGTTGAGTCTTTGATTCGGGCAAAACCAACCGCTGTGTAGCGGTG 4566
Qy 3662 GTTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAGGATCTCAAGAGATCCCTT 3721
Db 4565 GTTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAGGATCTCAAGAGATCCCTT 4506
Qy 3722 TGATCTTTTCTACGGGCTCTGACGCTCAGTGGAAACGAAACCTCAGCTTAAGGATTTTGG 3781
Db 4505 TGATCTTTTCTACGGGCTCTGACGCTCAGTGGAAACGAAACCTCAGCTTAAGGATTTTGG 4446
Qy 3782 TCAATGAGATTATC----- 3794
Db 4445 TCAATGAGATTATCAAAAAGGATCTTCACCTAGATCCTTTTAAATTAATAAGATTTTAA 4386
Qy 3795 -----GTGACCA 3802
Db 4385 GCACGTGTCAAGTCTCTCGGCCACGAAGTGACAGGATTGCGGCGGGGTGCGCA 4326
Qy 3803 AAGCGGCCATCGTGTCTCCCACTCTGCAAGTTTCGGGGGCATGGATGCGCGGATAGCGC 3862
Db 4325 GGGCGAACTCCCGCCCCACCGCTGCTCGCGATCTCGGTATGCGCGGCCCGGAGCGT 4266
Qy 3863 TGTGTGTTCTGAGATGCGCAGCGGATTTGCACTGCGCGGTAGAACTCCGCGAGGTGCTCCA 3922
Db 4265 CCGGGAAGTTCGTGGACACGACCTCGGACCACTCGGCGCTACAGCTCGTCAGGCGCGCA 4206
Qy 3923 GCC----- 3925

Db 4205 CCCACACCCAGCGCAGGGTGTGTTCGGCACCACTGGTCTGGACCGGCTGATGAACA 4146
Qy 3926 ---TCAGGACAGCTGAACCAACTCGCGAGGGGATCGAGCCGGGTGGCGAGAACT 3982
Db 4145 GGGTCACTGTCGTCGCGGACCAACCGGCGAAGTCGTCCTCCACGAAGTCCCGGGGAACC 4086
Qy 3983 CCAGCATGAGATCCCGCGCTGGAGATCATCCAGCGGCTCCCGGAAACGATTTCCA 4042
Db 4085 CGAGCCGCTCGTTCAGAACTCGACCGCTCGCGGACGTCGCGCGGTGAGCAACGGAA 4026
Qy 4043 AGCCCAACCTTTTCATAGAAAGCGCGGTGAATCGAAATCTCGTATGCGAGTTGGGG 4102
Db 4025 CGGACTGGTCACTTGGCCATGGTGGCCCTCTCAGTGTATTATTGAAGCATTTATC 3966
Qy 4103 TCGCTTGGTTCGCTCACTTTTGAACCCCGAGTCCCG----- 4137
Db 3965 AGGGTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAACAATAAG 3906
Qy 4138 ----- 4137
Db 3905 GGGTTCGCGCACATTTCCCGAAAAAGTGCACCTGTATGCGGTGTGAAATACCGCACAG 3846
Qy 4138 -----CTCAGAAGAACTC 4150
Db 3845 ATGCGTAAGGAGAAATACCGCATCAGGAAATTGTAAGGTTAATAATTCAGAAGAACTC 3786
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Db 3785 GTCAAGAAAGGCGATAGAAGCGGATCGCTGCGAAATCGGAGCGCGGATACCGTAAAGCA 3726
Qy 4211 GAGGAAGCGGTGAGCGCATTCGCGCGCAAGCTTTCAGCAATATCACGGGTAGCAACGC 4270
Db 3725 GAGGAAGCGGTGAGCGCATTCGCGCGCAAGCTTTCAGCAATATCACGGGTAGCAACGC 3666
Qy 4271 TATGTCTCTGATAGCGGTCCGCGCACACCGCGGCGCACAGTCCATGAATTCAGAAAGCG 4330
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Db 3605 GCCATTTTCCACCATGATATTCGGCAAGCGCATCGGCATCGGCATCGAGATTCCTC 3546
Qy 4391 GCGCTGCGGCATCGCGCTTGAGCTCGGCAAGAGTTTCGGCTGCGGCGGAGCCCTGATG 4450
Db 3545 GCGCTGCGGCATCGCTGCGCTTGAGCTTGCGCAAGAGTTTCGGCTGCGGCGGAGCCCTGATG 3486
Qy 4451 CTCTTCTGTCAGATCATCTGATCGACAAAGACCGGCTTCATCCGAGTACGTGCTCGCTC 4510
Db 3485 CTCTTCTGTCAGATCATCTGATCGACAAAGACCGGCTTCATCCGAGTACGTGCTCGCTC 3426
Qy 4511 GATGCGATGTTTTCGTTGGTTCGAAATGGGCGAGTAGCCGATCAAGCGTATGACGCG 4570
Db 3425 GATGCGATGTTTTCGTTGGTTCGAAATGGGCGAGTAGCCGATCAAGCGTATGACGCG 3366
Qy 4571 CGCATTTGATCAGCCATGATGATACCTTCTCGCAGGAGCAAGTTCGATGAGTAGAGAG 4630
Db 3365 CGCATTTGATCAGCCATGATGATACCTTCTCGCAGGAGCAAGTTCGATGAGTAGAGAG 3306
Qy 4631 ATCTGCCCCCGGCACTTCGCCCAATAGCAGCCAGTCCCTTCCCGCTTCAGTCAACAACGTC 4690
Db 3305 ATCTGCCCCCGGCACTTCGCCCAATAGCAGCCAGTCCCTTCCCGCTTCAGTCAACAACGTC 3246
Qy 4691 GAGCAAGCTGTCGCAAGGAAACCGCTGCTGTGCGCAGCAAGTATGCGCGCTGCTCGTC 4750
Db 3245 GAGCAAGCTGTCGCAAGGAAACCGCTGCTGTGCGCAGCAAGTATGCGCGCTGCTCGTC 3186
Qy 4751 CTGCAAGTTCAATTCAGGGCACCGGACAGGTTCGCTTTGACAAAAGAACCGGGCGCCCTG 4810
Db 3185 TTGCAAGTTCAATTCAGGGCACCGGACAGGTTCGCTTTGACAAAAGAACCGGGCGCCCTG 3126
Qy 4811 CGCTCAAGCCGGAACACGCGGCGCATCAGAGCAGCGGATGTTGTTGTTGCCAGTCAATA 4870
Db 3125 CGCTCAAGCCGGAACACGCGGCGCATCAGAGCAGCGGATGTTGTTGTTGCCAGTCAATA 3066

QY 3981 CTCCAGCATGATCCCGCGCTGGAGGATCATCCAGCGCGGTCCCGAACAACGATTCC 4040
Db 1674 CTCACGATGATCCCGCGCTGGAGGATCATCCAGCGCGGTCCCGAACAACGATTCC 1615
QY 4041 GAAGCCCAACCTTTTCATAGAAGCGCGGTGGAATCGAAATCTCGTGATGCGAGGTGGG 4100
Db 1614 GAAGCCCAACCTTTTCATAGAAGCGCGGTGGAATCGAAATCTCGTGATGCGAGGTGGG 1555
QY 4101 CGTCGCTTGGTCGGTCAATTCGAACCCCAAGATCCCGCTCAGAAGAACTCGTCAAGAAGG 4160
Db 1554 CGTCGCTTGGTCGGTCAATTCGAACCCCAAGATCCCGCTCAGAAGAACTCGTCAAGAAGG 1495
QY 4161 CGATAGAAGCGCATCGCGTCCGAATCGGAGCGCGGATACCGTAAAGCAAGGAGGAGCGG 4220
Db 1494 CGATAGAAGCGCATCGCGTCCGAATCGGAGCGCGGATACCGTAAAGCAAGGAGGAGCGG 1435
QY 4221 TCAGCCCATTCGCGCCCAAGCTCTTCAGCAATATACAGGGTAGCCAAACGCTATGTCCTGA 4280
Db 1434 TCAGCCCATTCGCGCCCAAGCTCTTCAGCAATATACAGGGTAGCCAAACGCTATGTCCTGA 1375
QY 4281 TAGCGTCCGCCACACCCAGCGGCCACAGTCGATGAATCCAGAAAGCGGCAATTTCC 4340
Db 1374 TAGCGTCCGCCACACCCAGCGGCCACAGTCGATGAATCCAGAAAGCGGCAATTTCC 1315
QY 4341 ACCATGATATTCGGCAAGCAGCATCGCCATGGGTACGACGAGATCCTCGCGTCGGC 4400
Db 1314 ACCATGATATTCGGCAAGCAGCATCGCCATGGGTACGACGAGATCCTCGCGTCGGC 1255
QY 4401 ATCGCGCTTGGCTGAGCTGCGCAACAGTTCGGCTGGCGGAGCCCTGATGCTCTTCGTC 4460
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QY 4461 AGATCATCTCGATTCGAAGAAGCGGCTTCATCCGAGTACGTCTCGCTCGATGCGATGT 4520
Db 1194 AGATCATCTCGATTCGAAGAAGCGGCTTCATCCGAGTACGTCTCGCTCGATGCGATGT 1135
QY 4521 TTGCTTGGTGGTTCGATGGCGAGGTAGCGGATCAAGCGTATGACGCGCGCATGCA 4580
Db 1134 TTGCTTGGTGGTTCGATGGCGAGGTAGCGGATCAAGCGTATGACGCGCGCATGCA 1075
QY 4581 TCAGCCATGATGATCTTTCTCGCAGGAGCAAGGTGAGATGACAGAGATCCTGCCCC 4640
Db 1074 TCAGCCATGATGATCTTTCTCGCAGGAGCAAGGTGAGATGACAGAGATCCTGCCCC 1015
QY 4641 GGCATCTCGCCCAATAGCAGCCAGTCCCTTCGCTTCAGTGACAAAGTTCGAGCAAGCT 4700
Db 1014 GGCATCTCGCCCAATAGCAGCCAGTCCCTTCGCTTCAGTGACAAAGTTCGAGCAAGCT 955
QY 4701 GCGCAAGGACGCGCTCGTGGCCAGCCAGTACGCGCGCTGCTCGTCCGATTTCA 4760
Db 954 GCGCAAGGACGCGCGCTCGTGGCCAGCCAGTACGCGCGCTGCTCGTCCGATTTCA 895
QY 4761 TTCAGGCGACCGGACAGGTGCGTCTTGACAAAAGAACCGGGCGCCCTCGCGCTGACAGC 4820
Db 894 TTCAGGCGACCGGACAGGTGCGTCTTGACAAAAGAACCGGGCGCCCTCGCGCTGACAGC 835
QY 4821 CGGAACAACGCGCATCAGAGCAGCGATTTGCTGTGTGTCGCCAGTCATAGCCGAATAGC 4880
Db 834 CGGAACAACGCGCATCAGAGCAGCGATTTGCTGTGTGTCGCCAGTCATAGCCGAATAGC 775
QY 4881 CTCTCCACCAAGCGCGGAGAACCTGCGTGAATCCATCTTGTTCAATCATGCGAAAC 4940
Db 774 CTCTCCACCAAGCGCGGAGAACCTGCGTGAATCCATCTTGTTCAATCATGCGAAAC 715
QY 4941 GATCCTCATCTCTCTTCATCAGATCTTTGATCCCTTCGCCCATCAGATCCTTGGCGGC 5000
Db 714 GATCCTCATCTCTCTTCATCAGATCTTTGATCCCTTCGCCCATCAGATCCTTGGCGGC 655
QY 5001 AAGAAAGCCATCAGTTTACTTTGCAAGGCTTCCCAACCTTACACAGGCGGCCCGAGCT 5060
Db 654 AAGAAAGCCATCAGTTTACTTTGCAAGGCTTCCCAACCTTACACAGGCGGCCCGAGCT 595

QY 5061 GCGAATTCGGTTCGCTGTGTCATAAAAACCCAGTCAGTATCGCATGTAAGC 5120
Db 594 GCGAATTCGGTTCGCTGTGTCATAAAAACCCAGTCAGTATCGCATGTAAGC 535
QY 5121 CCATGCAAGCTACCTGCTTTCTTTGCGCTTGGGTTTCCCTTGTCCAGATAGCCAG 5180
Db 534 CCATGCAAGCTACCTGCTTTCTTTGCGCTTGGGTTTCCCTTGTCCAGATAGCCAG 475
QY 5181 TAGCTGACATTCATCCGGGGTCAGACCGTTTCTCGGACTGGCTTCTACGTGTTCCGC 5240
Db 474 TAGCTGACATTCATCCGGGGTCAGACCGTTTCTCGGACTGGCTTCTACGTGTTCCGC 415
QY 5241 TTCTTTTAGCAGCCCTTCGCGCTTCAGTGTCTTGGGCAAGCGTG 5283
Db 414 TTCTTTTAGCAGCCCTTCGCGCTTCAGTGTCTTGGGCAAGCGTG 372
RESULT 11
ABQ78294
ID ABQ78294 standard; DNA; 2192 BP.
XX
AC ABQ78294;
XX
DT 05-NOV-2002 (first entry)
XX
DE Nucleotide sequence of plasmid pVC0289.
XX
KW Pig; growth hormone releasing hormone; GHRH; growth rate; lean body mass;
KW Insulin-like Growth Factor-I; IGF-I; milk production; feed efficiency;
KW somatotroph; growth-related disorder; hypopituitary dwarfism;
KW meat production; egg production; ss.
XX
OS Synthetic.
XX
PN WO200261037-A2.
XX
PD 08-AUG-2002.
XX
PF 12-DEC-2001; 2001WO-US048726.
XX
PR 12-DEC-2000; 2000US-0255021P.
XX
PA (BAYU) BAYLOR COLLEGE MEDICINE.
XX
PI (ADVI-) ADVISYS.
XX
PI Schwartz RJ, Carpenter RH, Draghia-Akli R, Kern DR, Smith RG;
XX
DR WPI; 2002-619237/66.
XX
PT Improving or enhancing growth, lean body mass, milk production, feed
PT efficiency or Insulin-like Growth Factor-I levels, comprises introducing
PT a vector encoding a growth hormone releasing hormone into an animal
PT before or during gestation.
XX
PS Example 2; Page 111-112; 113pp; English.
XX
CC The present sequence represents plasmid pVC0289, which was used to create
CC a vector carrying cDNA encoding pig growth hormone releasing hormone
CC (GHRH) cDNA. Nucleic acids encoding GHRH are used in the method of the
CC invention. The specification describes a method for improving or
CC enhancing characteristics e.g. growth, lean body mass, Insulin-like
CC Growth Factor (IGF)-I levels, growth rate and milk production in an
CC offspring, and for delaying birth of an offspring. The method comprises
CC introducing a vector, encoding GHRH, into cells of the female animal
CC prior to or during gestation of the offspring under conditions where the
CC nucleotide sequence is expressed. The method is useful of improving or
CC enhancing animal growth, for increasing growth hormone, lean body mass,
CC IGF-I levels, feed efficiency, growth rate, ratio of somatotrophs to
CC other hormone-producing cells in a pituitary gland, and milk production
CC in an offspring, and for delaying birth of an offspring. GHRH nucleic
CC acids and vectors are used for diagnostic purposes in clinical medicine,
CC both human and veterinary, e.g. in treating growth-related disorders such
CC as hypopituitary dwarfism resulting from abnormalities in growth hormone

CC production, and in stimulating the growth and enhancing feed conversion
CC efficiency of animals raised for meat, milk and egg production
XX
SQ Sequence 2192 BP; 486 A; 634 C; 601 G; 471 T; 0 U; 0 Other;
Query Match 30.48; Score 1603.8; DB 6; Length 2192;
Best Local Similarity 82.88; Pred. No. 2.6e-234;
Matches 2022; Conservative 0; Mismatches 27; Indels 392; Gaps 1;
QY 2706 CTAGACGTAATCATAGTGTATAGTGTCTCTGTGTGAAATGTATCCGCTCACAATTC 2765
DB 70 CTTGGCGTAATCATGGTCATAGTGTCTCTGTGTGAAATGTATCCGCTCACAATTC 129
QY 2766 ACACCAATACGAGCCGGAAGCAATAAGTGTAAAGCTGGGGTCCCTTAATGAGTGAGCTA 2825
DB 130 ACACCAATACGAGCCGGAAGCAATAAGTGTAAAGCTGGGGTCCCTTAATGAGTGAGCTA 189
QY 2826 ACTCACATTAATTTGGCTTGGCTCACTGCCCGCTTCCAGTCGGGAACCTGTGCGCA 2885
DB 190 ACTCACATTAATTTGGCTTGGCTCACTGCCCGCTTCCAGTCGGGAACCTGTGCGCA 249
QY 2886 GCTGCATTAATTAATCGGCCAAACGCGCGGAGAGCGGTTTCGCTATTGGGCGCTTTC 2945
DB 250 GCTGCATTAATTAATCGGCCAAACGCGCGGAGAGCGGTTTCGCTATTGGGCGCTTTC 309
QY 2946 CGCTTCTCGCTCACTGACTCGCTGCGCTCGGTTCGCTCGCGGAGCGGTATCAGC 3005
DB 310 CGCTTCTCGCTCACTGACTCGCTGCGCTCGGTTCGCTCGCGGAGCGGTATCAGC 369
QY 3006 TCACCTAAAGCCGTAATACGGTTATCCACAGAAATCAGGGGATAACGCGAGGAAGCAAT 3065
DB 370 TCACCTAAAGCCGTAATACGGTTATCCACAGAAATCAGGGGATAACGCGAGGAAGCAAT 429
QY 3066 GTGAGCAAAAGGCGCAGCAAAAGGCCAGGAACCGTAAAGGCCGCGTTCGTCGCGTTT 3125
DB 430 GTGAGCAAAAGGCGCAGCAAAAGGCCAGGAACCGTAAAGGCCGCGTTCGTCGCGTTT 489
QY 3126 CCATAGGCTCCGCCCCCTGACGAGCATCAAAAAATCGACGCTCAAGTCAGAGGTGGG 3185
DB 490 CCATAGGCTCCGCCCCCTGACGAGCATCAAAAAATCGACGCTCAAGTCAGAGGTGGG 549
QY 3186 AAACCCGACAGACTATAAGATACAGGGGTTCCCGCTGGAAGTCCCTGTGGGCTC 3245
DB 550 AAACCCGACAGACTATAAGATACAGGGGTTCCCGCTGGAAGTCCCTGTGGGCTC 609
QY 3246 TCTGTTCGACCTCCGCTTACCGGATACCTGTCCGCTTTCCTCCCTCGGAGCGT 3305
DB 610 TCTGTTCGACCTCCGCTTACCGGATACCTGTCCGCTTTCCTCCCTCGGAGCGT 669
QY 3306 GGCGCTTCTCATPAGCTCAGCTGTAGGTATCTCAGTTCGGTGTAGGTGCTTCGCTCCAA 3365
DB 670 GGCGCTTCTCATPAGCTCAGCTGTAGGTATCTCAGTTCGGTGTAGGTGCTTCGCTCCAA 729
QY 3366 GCTGGGCTGTGCAAGAACCCCGCTTACGCGGACCGGTGCGCTTATCCGGTAACTA 3425
DB 730 GCTGGGCTGTGTCAGCAACCCCGCTTACGCGGACCGGTGCGCTTATCCGGTAACTA 789
QY 3426 TCGTCTTGAGTCCAAACCCGTAAGACACGCTTATCGCACCTGGCAGAGCCACTGGTAA 3485
DB 790 TCGTCTTGAGTCCAAACCCGTAAGACACGCTTATCGCACCTGGCAGAGCCACTGGTAA 849
QY 3486 CAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCCTTGAAGTGGTGGCTAA 3545
DB 850 CAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCCTTGAAGTGGTGGCTAA 909
QY 3546 CTACGGCTACCTAGAGAACAGTATTTGGTATCTCGCTCTGCTGAAGCCAGTACCTT 3605
DB 910 CTACGGCTACCTAGAGAACAGTATTTGGTATCTCGCTCTGCTGAAGCCAGTACCTT 969
QY 3606 CGGAAAAAGTGTGTAGCTCTTGATCCGCAACCAACCCGCTGGTGGTGGGTTT 3665
DB 970 CGGAAAAAGTGTGTAGCTCTTGATCCGCAACCAACCCGCTGGTGGTGGGTTT 1029

QY 3666 TTTTGTTCAGACGACAGATTACGCGCAGAAAAAAGGATCTCAAGAGATCCTTTGAT 3725
DB 1030 TTTTGTTCAGACGACAGATTACGCGCAGAAAAAAGGATCTCAAGAGATCCTTTGAT 1089
QY 3726 CTTTTCACGGGTCAGCGCTCAGTGGAAACGAAACTCACGTTAAGGGATTTTGGTCAT 3785
DB 1090 CTTTTCACGGGTCGTA----- 1107
QY 3786 GAGATTATCGTCAGAACAAAGCGGCATCGTGCCTCCCACTCTCGCAGTTCGGGGGCGATG 3845
DB 1108 ----- 1107
QY 3846 GATGCGCGATAGCCGCTCTCTGTTTCTTGGATGCCGACGGAATTTGCACTGCCGCTAGAA 3905
DB 1108 ----- 1107
QY 3906 CTCGCGGAGTCTGTCAGGCTCAGGCGAGCTGAACCAACTCGCGAGGGGATCGAGCCC 3965
DB 1108 ----- 1107
QY 3966 GGGTGGCGAAGAACTCCAGCATGAGATCCCGGCTGAGGATCATCCAGCCGGCGTC 4025
DB 1108 ----- 1107
QY 4026 CCGGAAAAAGATTCGGAAGCCCAACCTTTATAGAAGCGCGGTGGAATTCGAAATCTCG 4085
DB 1108 ----- 1107
QY 4086 TGATGCGAGTTGGGCTCGCTTGGTTCGTCATTTTCGAACCCCAAGATCCCGCTCAGAAG 4145
DB 1108 -----CGCTCAGAAG 1117
QY 4146 AACTCGTCAAGAGCGATAGAAGCGATCGCTCGAATCGGAGCGCGATACCGTAA 4205
DB 1118 AACTCGTCAAGAGCGATAGAAGCGATCGCTCGAATCGGAGCGCGATACCGTAA 1177
QY 4206 AGCAGGAGAACGGTCAGCCCATTCGCGCCCAAGCTCTTCAGCAATATCAGGGTAGCC 4265
DB 1178 AGCAGGAGAACGGTCAGCCCATTCGCGCCCAAGCTCTTCAGCAATATCAGGGTAGCC 1237
QY 4266 AACGCTATGCTCTGATAGCGTCCGCCACACCCAGCGGCCACAGTCGATGAATCCAGAA 4325
DB 1238 AACGCTATGCTCTGATAGCGTCCGCCACACCCAGCGGCCACAGTCGATGAATCCAGAA 1297
QY 4326 AAGCGSCCATTTTCCACATGATATTCGCAAGAGGATTCGCCATGGGTCAAGCGACA 4385
DB 1298 AAGCGSCCATTTTCCACATGATATTCGCAAGAGGATTCGCCATGGGTCAAGCGACA 1357
QY 4386 TCCTCGCGTCGCGCATCGCGCTTGAGCCCTTGCGCAACAGTTCGCGCTGGCGGAGCCCC 4445
DB 1358 TCCTCGCGTCGCGCATCGCGCTTGAGCCCTTGAGCCCTTGCGCAACAGTTCGCGCTGGCGGAGCCCC 1417
QY 4446 TGATGCTCTTCTGTCAGATCATCTGATCGCAAGACCGGCTTCATCCAGTACGTCGT 4505
DB 1418 TGATGCTCTTCTGTCAGATCATCTGATCGCAAGACCGGCTTCATCCAGTACGTCGT 1477
QY 4506 CGCTCGATGCGATGTTTCGCTGGTGTGATGGGAGGATAGCGGATCAAGCGTATGC 4565
DB 1478 CGCTCGATGCGATGTTTCGCTGGTGTGATGGGAGGATAGCGGATCAAGCGTATGC 1537
QY 4566 AGCCCGCCGATTCGATCAGCCATGATGATCTTTCTCGGAGGAGCAAGGTGAGATGAC 4625
DB 1538 AGCCCGCCGATTCGATCAGCCATGATGATCTTTCTCGGAGGAGCAAGGTGAGATGAC 1597
QY 4626 AGGAGATCTTCCCGGCACTTCGCCCCAATAGCAGCCAGTCCCTTCCCGCTTCAGTGACA 4685
DB 1598 AGGAGATCTTCCCGGCACTTCGCCCCAATAGCAGCCAGTCCCTTCCCGCTTCAGTGACA 1657
QY 4686 AGCTCGACACAGCTGCGCAAGGACCCCGCTGTCGCGCACCCAGATAGCGCGCTGCC 4745
DB 1658 AGCTCGACACAGCTGCGCAAGGACCCCGCTGTCGCGCACCCAGATAGCGCGCTGCC 1717
QY 4746 TCGTCTCGAGTTCATTTCAGGGGACCGGACAGGTCCGTCTTTGACAAAAAAGAACCGGGCGC 4805

|||||
1718 TGTCTCTGAGTTCATTAGGGCACCGGACAGTGGTCTTGACAAAAGAACCGGGCGC 1777
QY 4806 CCTGCGCTGACAGCGGGAACACGGCGGCATCAGAGCAGCCGATTGTCTGTGTGCCACG 4865
Db 1778 CCTGCGCTGACAGCGGGAACACGGCGGCATCAGAGCAGCCGATTGTCTGTGTGCCACG 1837
QY 4866 TCATAGCCGAATAGCTCTCCACCACGCGGCGGAGAACCTGCGTGCAATCCATCTTGT 4925
Db 1838 TCATAGCCGAATAGCTCTCCACCACGCGGCGGAGAACCTGCGTGCAATCCATCTTGT 1897
QY 4926 TCAATCATCGAAACGATCCTCATCTGTCTCTGTGATCAGATCTTGATCCCTCGGCCAT 4985
Db 1898 TCAATCATCGAAACGATCCTCATCTGTCTCTGTGATCAGATCTTGATCCCTCGGCCAT 1957
QY 4986 CAGATCTTTGGCGGCAAGAACCCATCCAGTTTACTTTTCAGGGCTTCCCAACCTTACCA 5045
Db 1958 CAGATCTTTGGCGGCAAGAACCCATCCAGTTTACTTTTCAGGGCTTCCCAACCTTACCA 2017
QY 5046 GAGGGGCGCCAGCTGGGAATTCGGGTTCGCTTGTCTGTGTCATTAATAAACCGCCAGCTTAGC 5105
Db 2018 GAGGGGCGCCAGCTGGGAATTCGGGTTCGCTTGTCTGTGTCATTAATAAACCGCCAGCTTAGC 2077
QY 5106 TATCGCCATGTAAGCCCACTGCAAGCTACCTGCTTCTCTT 5146
Db 2078 AACTGTTGGGAAGGGCGATCGGTGGGGCTCTTTCGCTAATT 2118

RESULT 12

ABQ78293
ID ABQ78293 standard; DNA; 3534 BP.
XX AC ABQ78293;
XX DT 05-NOV-2002 (first entry)
XX DE Nucleotide sequence of vector pSPc5-12-HV-GHRH.
XX KW Pig; growth hormone releasing hormone; GHRH; growth rate; lean body mass;
KW Insulin-like Growth Factor-I; IGF-I; milk production; feed efficiency;
KW somatotroph; growth-related disorder; hypopituitary dwarfism;
KW meat production; egg production; ss.
XX Synthetic.
XX OS
XX PN WO200261037-A2.
XX PD 08-AUG-2002.
XX PF 12-DEC-2001; 2001WO-US048726.
XX PR 12-DEC-2000; 2000US-0255021P.
XX PA (BAYU) BAYLOR COLLEGE MEDICINE.
XX PA (ADVI-) ADVISYS.
XX PI Schwartz RJ, Carpenter RH, Draghia-Akli R, Kern DR, Smith RG;
XX WPI; 2002-619237/66.
XX PT Improving or enhancing growth, lean body mass, milk production, feed
PT efficiency or insulin-like Growth Factor-I levels, comprises introducing
PT a vector encoding a growth hormone releasing hormone into an animal
PT before or during gestation.
XX PS Example 2; Page 109-111; 113pp; English.
XX CC The present sequence represents vector pSPc5-12-HV-GHRH, which carries
CC cDNA encoding pig growth hormone releasing hormone (GHRH) cDNA. Nucleic
CC acids encoding GHRH are used in the method of the invention. The
CC specification describes a method for improving or enhancing
CC characteristics e.g. growth, lean body mass, insulin-like Growth Factor
CC (IGF)-I levels, growth rate and milk production in an offspring, and for

CC delaying birth of an offspring. The method comprises introducing a
CC vector, encoding GHRH, into cells of the female animal prior to or during
CC gestation of the offspring under conditions where the nucleotide sequence
CC is expressed. The method is useful of improving or enhancing animal
CC growth, for increasing growth hormone, lean body mass, IGF-I levels, feed
CC efficiency, growth rate, ratio of somatotrophs to other hormone-producing
CC cells in a pituitary gland, and milk production in an offspring, and for
CC delaying birth of an offspring. GHRH nucleic acids and vectors are used
CC for diagnostic purposes in clinical medicine, both human and veterinary,
CC e.g. in treating growth-related disorders such as hypopituitary dwarfism
CC resulting from abnormalities in growth hormone production, and in
CC stimulating the growth and enhancing feed conversion efficiency of
CC animals raised for meat, milk and egg production
XX
SQ Sequence 3534 BP; 764 A; 1018 C; 979 G; 773 T; 0 U; 0 Other;
Query Match 30.4%; Score 1603.8; DB 6; Length 3534;
Best Local Similarity 82.8%; Pred. No. 2.5e-234;
Matches 2022; Conservative 0; Mismatches 27; Indels 392; Gaps 1;
QY 2706 CTAGACGTAATCATGGTCAATAGCTGTTTCTCTGTGTGAAATTTGTTATCCGCTCACAAATCC 2765
Db 1412 CTTGGCGTAATCATGGTCAATAGCTGTTTCTCTGTGTGAAATTTGTTATCCGCTCACAAATCC 1471
QY 2766 ACACAACATACGAGCGGAGCATAAAGTGTAAAGCCTGGGTGCTTAATGAGTGAGCTA 2825
Db 1472 ACACAACATACGAGCGGAGCATAAAGTGTAAAGCCTGGGTGCTTAATGAGTGAGCTA 1531
QY 2826 ACTCATTAATTTGCGTTGCGCTCACTGCCGCTTTTCCAGTGGGAAACCTGTCTGTGCCA 2885
Db 1532 ACTCATTAATTTGCGTTGCGCTCACTGCCGCTTTTCCAGTGGGAAACCTGTCTGTGCCA 1591
QY 2886 GCTGCAATTAATGAATCGGCCAAACGGCGGGGAGAGCGGTTTGCATTTGGCGCTCTTC 2945
Db 1592 GCTGCAATTAATGAATCGGCCAAACGGCGGGGAGAGCGGTTTGCATTTGGCGCTCTTC 1651
QY 2946 GCCTTCTCGCTCACTGACTCGCTCGCTCGCTCGCTCGCGGAGCGGTTATCAGC 3005
Db 1652 GCCTTCTCGCTCACTGACTCGCTCGCTCGCTCGCTCGCGGAGCGGTTATCAGC 1711
QY 3006 TCACCTCAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCGAGAAAGAACAT 3065
Db 1712 TCACCTCAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCGAGAAAGAACAT 1771
QY 3066 GTGAGCAAAAGCCAGCAAAAGCCAGGAACCGTAAAAAGGCCGCTTGTGCGCGCTTTT 3125
Db 1772 GTGAGCAAAAGCCAGCAAAAGCCAGGAACCGTAAAAAGGCCGCTTGTGCGCGCTTTT 1831
QY 3126 CCATAGGCTCGCGCCCTCGACGAGCATCACAATAATCGACCTCAAGTCAGAGGTGGCG 3185
Db 1832 CCATAGGCTCGCGCCCTCGACGAGCATCACAATAATCGACCTCAAGTCAGAGGTGGCG 1891
QY 3186 AAACCCGACAGGACTATAAAGATACAGCGGTTTCCCGCTTGAAGCTCCCTCGTGGCTC 3245
Db 1892 AAACCCGACAGGACTATAAAGATACAGCGGTTTCCCGCTTGAAGCTCCCTCGTGGCTC 1951
QY 3246 TCCTGTTCCGACCTTCACCGATACCTGTCCGCTTTCCTTCCCTTCGCGAAGCT 3305
Db 1952 TCCTGTTCCGACCTTCACCGATACCTGTCCGCTTTCCTTCCCTTCGCGAAGCT 2011
QY 3306 GCGGCTTCTCATAGCTACGCTGATGATATCTCAGTTTCGGGTGATAGTTCGCTCCAA 3365
Db 2012 GCGGCTTCTCATAGCTACGCTGATGATATCTCAGTTTCGGGTGATAGTTCGCTCCAA 2071
QY 3366 GCTGGGCTGTGTGCACGAACCCCGCTTCAGCCGACCGCTCGGCTTATCCGGTAACCTA 3425
Db 2072 GCTGGGCTGTGTGCACGAACCCCGCTTCAGCCGACCGCTCGGCTTATCCGGTAACCTA 2131
QY 3426 TCGCTTGTAGTCAACCCCGGTAAAGACACGACTTATGCCACCTGGCAGCAGCCACTGGTAA 3485
Db 2132 TCGCTTGTAGTCAACCCCGGTAAAGACACGACTTATGCCACCTGGCAGCAGCCACTGGTAA 2191
QY 3486 CAGGATTACAGAGCGAGGTATGTAGGCGGTCTACAGAGTTCTTGAAAGTGTGGGCTTAA 3545

Db 2192 CAGGATTAGCAGAGCGAGGTATGTAGCGGTGCTACAGAGTTCTTGAAGTGGTGGCTAA 2251
QY 3546 CTACGGCTTACACTAGAGAAACAGTATTGGTATCTGGCTCTGTGAAGCCAGTTACCTT 3605
Db 2252 CTACGGCTTACACTAGAGAAACAGTATTGGTATCTGGCTCTGTGAAGCCAGTTACCTT 2311
QY 3606 CGGAAAAGAGTTGGTACTTCTGATCCGGCAAAACAAACCCCTGGTAGCGGTGTTT 3665
Db 2312 CGGAAAAGAGTTGGTACTTCTGATCCGGCAAAACAAACCCCTGGTAGCGGTGTTT 2371
QY 3666 TTTTGTGTTGCAAGCAGCAGATTACGCGCAGAAAAGAGTCTCAAGAGATCCTTTGAT 3725
Db 2372 TTTTGTGTTGCAAGCAGCAGATTACGCGCAGAAAAGAGTCTCAAGAGATCCTTTGAT 2431
QY 3726 CTTTCTTACCGGGTCTCAGCTCAGTGGAAAGAACTCAGTTAAGGGATTTTGGTCA 3785
Db 2432 CTTTCTTACCGGGTCTCA 2449
QY 3786 GAGATTATCGTCGACCAAGCGGCATCGTGCTTCCCACTCTCTGCAAGTTGCGGGGCATG 3845
Db 2450 2449
QY 3846 GATCGCGGATAGCGCTGCTGTTTCTTGATGCCAGAGTTTGCACTGCCCGGTAGAA 3905
Db 2450 2449
QY 3906 CTCGCGAGGTTCGTCAGCCTCAGCAGCAGTGAACCACTCGCAGGGGATCGAGCCC 3965
Db 2450 2449
QY 3966 GGGTGGGCGAAGAACTCCAGCATGAGATCCCGCGCTGGAGGATCATCCAGCGGGCTC 4025
Db 2450 2449
QY 4026 CCGGAAAACGATCCGGAAGCCCAACCTTTCATAGAAGCGCGGTGGAATCGAAATCTCG 4085
Db 2450 2449
QY 4086 TGATGCGAGTTGGGCGTCTGGTGGTCAATTTCCGACCCAGAGTCCCGCTCAGAAG 4145
Db 2450 2459
QY 4146 AACTCGTCAAGAGGCGATAGAGGCGATGCGTTCGAATCGGAGCGGCGATACCGTAA 4205
Db 2460 AACTCGTCAAGAGGCGATAGAGGCGATGCGTTCGAATCGGAGCGGCGATACCGTAA 2519
QY 4206 AGCAGGAGGAGCGGTGAGCCATTCGCCGCCAAGCTCTTCAGCAATATCACGGGTAGCC 4265
Db 2520 AGCAGGAGGAGCGGTGAGCCATTCGCCGCCAAGCTCTTCAGCAATATCACGGGTAGCC 2579
QY 4266 AACGCTATGCTGTAGAGCGTCCGCCACACCCAGCGGCGCACAGTCGATGAATCCAGAA 4325
Db 2580 AACGCTATGCTGTAGAGCGTCCGCCACACCCAGCGGCGCACAGTCGATGAATCCAGAA 2639
QY 4326 AAGCGGCCATTTCCACCATGATATTCGCAAGCAGGCATCGCATGGGTCAAGCAGAGA 4385
Db 2640 AAGCGGCCATTTCCACCATGATATTCGCAAGCAGGCATCGCATGGGTCAAGCAGAGA 2699
QY 4386 TCCTCGCGCTGGGCGATGCGCGCTTGAGCTCGCGCAACAGTTTCGGTGGCGCGAGCCCC 4445
Db 2700 TCCTCGCGCTGGGCGATGCGCGCTTGAGCTCGCGCAACAGTTTCGGTGGCGCGAGCCCC 2759
QY 4446 TGATGCTCTTGTCCAGATCATCTGATCGACAGACCGGCTTCATCCGAGTACGTGCT 4505
Db 2760 TGATGCTCTTGTCCAGATCATCTGATCGACAGACCGGCTTCATCCGAGTACGTGCT 2819
QY 4506 CGCTCGATCGATGTTTTCGCTTGTGTCGAATGGGCGAGTAGCCGATCAAGCGTATGC 4565
Db 2820 CGCTCGATCGATGTTTTCGCTTGTGTCGAATGGGCGAGTAGCCGATCAAGCGTATGC 2879
QY 4566 AGCGCGCGCATTCGATCAGCCATGATGATATCTTCTCGCAGGAGCAAGGTGAGATGAC 4625

Db 2880 AGCGCGCGCATTCGATCAGCCATGATGGATATCTTCTCGCAGGAGCAAGGTGAGATGAC 2939
QY 4626 AGGAGATCTCTGCCCGGCACTTCGCCCAATAGCAGCCAGTCCCTTCCCGCTTCAGTGACA 4685
Db 2940 AGGAGATCTCTGCCCGGCACTTCGCCCAATAGCAGCCAGTCCCTTCCCGCTTCAGTGACA 2999
QY 4686 ACCTCGAGCAACAGTTCGCGCAAGAACCCCGTCTGTGGCCAGCCACGATAGCCGCGTCC 4745
Db 3000 ACCTCGAGCAACAGTTCGCGCAAGAACCCCGTCTGTGGCCAGCCACGATAGCCGCGTCC 3059
QY 4746 TCCTCTCTGCAAGTTCATTCAGGGCACCGGACAGTCCGTCTTGACAAAAGAACCGGGCGC 4805
Db 3060 TCCTCTCTGCAAGTTCATTCAGGGCACCGGACAGTCCGTCTTGACAAAAGAACCGGGCGC 3119
QY 4806 CCCTGCGCTCACAGCGGCAACAGCGGCGCATCAGAGCAGCGATTGTCTGTGTGCCAG 4865
Db 3120 CCCTGCGCTCACAGCGGCAACAGCGGCGCATCAGAGCAGCGATTGTCTGTGTGCCAG 3179
QY 4866 TCATAGCGCAATAGCCTCTCCACCAGCGCGCGGAGAACCTCGTGCAATCCATCTTGT 4925
Db 3180 TCATAGCGCAATAGCCTCTCCACCAGCGCGCGGAGAACCTCGTGCAATCCATCTTGT 3239
QY 4926 TCATCATGCGAAACGATCTCATCTCTCTTGTGATCAGATCTTGTATCCCTGCGGCAT 4985
Db 3240 TCATCATGCGAAACGATCTCATCTCTCTTGTGATCAGATCTTGTATCCCTGCGGCAT 3299
QY 4986 CAGATCTTGGCGGCAAGAACGATCCAGTTCCTTGTGAGGCTTCCCAACCTTACCA 5045
Db 3300 CAGATCTTGGCGGCAAGAACGATCCAGTTCCTTGTGAGGCTTCCCAACCTTACCA 3359
QY 5046 GAGGCGCGCCAGCTGCGCAATTCGGTTCGCTTGTCTTCCATAAAACCGCCAGTCTAGC 5105
Db 3360 GAGGCGCGCCAGCTGCGCAATTCGGTTCGCTTGTCTTCCATAAAACCGCCAGTCTAGC 3419
QY 5106 TATGCGCATGTAAGCCACTGCAAGTACCTGCTTCTTCTT 5146
Db 3420 AACTGTTGGAGGCGGATCGGTGCGGCGCTCTTCGCTATT 3460

RESULT 13
AAL62060
ID AAL62060 standard; DNA; 3534 BP.
XX AAL62060;
AC AC
AT 22-SEP-2003 (first entry)
DT XX
TX TV-GHRH plasmid DNA.
DE Plasmid-mediated supplementation; anaemia; tumour; adenoma; melanoma;
XX sarcoma; immune dysfunction; carcinoma; leukaemia; kidney failure;
KW lymphoma; weight loss; lymphopoesis; appetite stimulant; anorectic;
KW growth hormone releasing hormone; GHRH; cyclic; circular; gene; ds.
XX Unidentified.
OS WO2003049700-A2.
XX PN 19-JUN-2003.
XX PD 10-DEC-2002; 2002WO-US039509.
XX PF 11-DEC-2001; 2001US-0339610P.
XX PR (ADVI-) ADVISYS INC.
PA (BAYU) BAYLOR COLLEGE MEDICINE.
XX PI Draghia-Akli R. Carpenter RH, Kern DR, Schwartz RJ, King G;
PI Hahn K, Brenner MK;
XX WPI; 2003-558968/52.
DR Treating anemia, immune dysfunction, tumor, increasing total red blood
PT

PT cell mass, reversing wasting or abnormal weight loss in subject, by
PT administering nucleic acid construct encoding growth-hormone-releasing-
PT hormone.

XX Claim 4; Page 193-195; 212pp; English.

XX The invention relates to compositions and methods for plasmid-mediated
CC supplementation. The method is useful for treating anaemia, tumour (such
CC as adenoma, mast cell tumour, melanoma, sarcoma or solid tumour), immune
CC dysfunction, carcinoma (benign or malignant), leukaemia, lymphoma or
CC kidney failure, for preventing the development of metastatic tumour, for
CC increasing total red blood cell mass, for reversing wasting, abnormal
CC weight loss or suppression of lymphopoiesis, in a subject, or for
CC increasing weight gain in a chronically ill subject or, or for extending
CC life expectancy for a chronically ill subject. The present sequence is IV
CC -growth hormone releasing hormone (GHRH) plasmid DNA. This sequence is
CC used to illustrate the method of the invention

XX Sequence 3534 BP; 764 A; 1016 C; 979 G; 775 T; 0 U; 0 Other;

Query Match 30.4%; Score 1603.8; DB 9; Length 3534;

Best Local Similarity 82.8%; Pred. No. 2.5e-234;

Matches 2022; Conservative 0; Mismatches 27; Indels 392; Gaps 1;

QY	2706	CTAGAGCTAATCATGTGTAGCTGTTTCTGTGTGAATTTGTTATCCGCTCACAATTCC	2765
DB	1412	CTTGGCGTAATCATGTGTAGCTGTTTCTGTGTGAATTTGTTATCCGCTCACAATTCC	1471
QY	2766	ACACAACATACGAGCGGAGCATAAAGTGTAAAGCTTGGGTGCCTAATGAGTGAGCTA	2825
DB	1472	ACACAACATACGAGCGGAGCATAAAGTGTAAAGCTTGGGTGCCTAATGAGTGAGCTA	1531
QY	2826	ACTCACATTAATTTGGTGTGGCTCACTGCCCGCTTTCAGTCGGGAAACCTGTGTGCCA	2885
DB	1532	ACTCACATTAATTTGGTGTGGCTCACTGCCCGCTTTCAGTCGGGAAACCTGTGTGCCA	1591
QY	2886	GCATGCAATTAATGAATCGGCCAAGCGCGGGAGAGCGGTTTCGTTATTTGGGCGCTTTC	2945
DB	1592	GCATGCAATTAATGAATCGGCCAAGCGCGGGAGAGCGGTTTCGTTATTTGGGCGCTTTC	1651
QY	2946	CGCTTCTCGCTCACTGACTCGTGTGGCTCGGTTCGGCTCGCGGAGCGGTATCAGC	3005
DB	1652	CGCTTCTCGCTCACTGACTCGTGTGGCTCGGTTCGGCTCGCGGAGCGGTATCAGC	1711
QY	3006	TCACCTAAAGCGGTAATACGGTTATCCACAGAAATCAGGGGATAACGACGAAAGAACAT	3065
DB	1712	TCACCTAAAGCGGTAATACGGTTATCCACAGAAATCAGGGGATAACGACGAAAGAACAT	1771
QY	3066	GTGAGCAAAAGGCCAGCAAAAGGCCAGAACCGTAAAGAGCGCGTTCGTCGGCGTTT	3125
DB	1772	GTGAGCAAAAGGCCAGCAAAAGGCCAGAACCGTAAAGAGCGCGTTCGTCGGCGTTT	1831
QY	3126	CCATAGGCTCCGCCCTCGACGAGCATCAAAAAATTCGACGCTCAAGTCAGAGGTGGCG	3185
DB	1832	CCATAGGCTCCGCCCTCGACGAGCATCAAAAAATTCGACGCTCAAGTCAGAGGTGGCG	1891
QY	3186	AAACCCGACAGGACTATAAAGATACAGGCGTTTCCCTCGAAGTTCCTCGTGGCTC	3245
DB	1892	AAACCCGACAGGACTATAAAGATACAGGCGTTTCCCTCGAAGTTCCTCGTGGCTC	1951
QY	3246	TCCTGTTCGACCTCGCGTTACCGATACCTGTCCGCTTCTCCCTCGGGAAGCGT	3305
DB	1952	TCCTGTTCGACCTCGCGTTACCGATACCTGTCCGCTTCTCCCTCGGGAAGCGT	2011
QY	3306	GGCGCTTCTCATAGCTCAGCGTGTAGGTATCTCAGTTCCGTTAGGTTCCTCGCTCCAA	3365
DB	2012	GGCGCTTCTCATAGCTCAGCGTGTAGGTATCTCAGTTCCGTTAGGTTCCTCGCTCCAA	2071
QY	3366	GCTGGGCTGTGTGACGAAACCCCGCTTACGCCGACCGCTGCGCTTATCCGGTAACCTA	3425
DB	2072	GCTGGGCTGTGTGACGAAACCCCGCTTACGCCGACCGCTGCGCTTATCCGGTAACCTA	2131
QY	3426	TCGTCTTGTAGTCCAAACCGGTAAGACACGACTTATCGCCACTGGCAGCACCCTGTGTA	3485

DB	2132	TGCTCTTGAGTCCAAACCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGTGTA	2191
QY	3486	CAGGATTAGCAGAGCGAGGTATGTAGCGGTGTACAGAGTTCTTGAAGTGTGGCTAA	3545
DB	2192	CAGGATTAGCAGAGCGAGGTATGTAGCGGTGTACAGAGTTCTTGAAGTGTGGCTAA	2251
QY	3546	CTACGGCTACACTAGAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTT	3605
DB	2252	CTACGGCTACACTAGAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTT	2311
QY	3606	CGGAAAAAGAGTTGGTAGTCTTTGATCCGGCAAAACAAACCCAGCTGTGTAGCGGTGTTT	3665
DB	2312	CGGAAAAAGAGTTGGTAGTCTTTGATCCGGCAAAACAAACCCAGCTGTGTAGCGGTGTTT	2371
QY	3666	TTTTGTTTCAAGCAGCAGATTAACGCGCAGAAAAAAGAGTCTCAAGAAAGATCTTTGAT	3725
DB	2372	TTTTGTTTCAAGCAGCAGATTAACGCGCAGAAAAAAGAGTCTCAAGAAAGATCTTTGAT	2431
QY	3726	CTTTTCTACGGGTCTGACGCTCAGTGGAAACGAAACCTCACGTTAAGGATTTTGGTCAT	3785
DB	2432	CTTTTCTACGGGTCTGAA-----	2449
QY	3786	GAGATTATCGTCGACCAAGCGGCATCGTGCCTCCCACTCCTGCAGTTCCGGGGCATG	3845
DB	2450	-----	2449
QY	3846	GATGCGGATAGCGCTGCTGTTTCTGGATGCGACGAGATTGTCATCTGCCGCTAGAA	3905
DB	2450	-----	2449
QY	3906	CTCCGCGAGTGTCTCAGGCTCAGGCAGCAGCTGAAACCACTCGCGAGGGATCGAGCCC	3965
DB	2450	-----	2449
QY	3966	GGGTTGGCGAAGAACTCCAGCATGAGATCCCGCGCTGGAGGATCATCAGCCGGCGTC	4025
DB	2450	-----	2449
QY	4026	CCGGAACAGTTCGAAAGCCCAACCTTTTCATAGAGGGCGGGTGGATTCGAAATCTCG	4085
DB	2450	-----	2449
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DB	2450	-----CGCTCAGAAG	2459
QY	4146	AATCTCTCAAGAGGCGATAGAGGCGATCGCTGCGAATTCGGAGCGGCGATACCGTAA	4205
DB	2460	AATCTCTCAAGAGGCGATAGAGGCGATCGCTGCGAATTCGGAGCGGCGATACCGTAA	2519
QY	4206	AGCAGGAAAGCGGTACGCCCATTCGCGCCCAAGCTCTTCAGCAATATCAGGGTAGCC	4265
DB	2520	AGCAGGAAAGCGGTACGCCCATTCGCGCCCAAGCTCTTCAGCAATATCAGGGTAGCC	2579
QY	4266	AAGCTATCTCTGATAGCGGTCCGCGCACACCCAGCGCGCCACAGTCGATGATCAGAA	4325
DB	2580	AAGCTATCTCTGATAGCGGTCCGCGCACACCCAGCGCGCCACAGTCGATGATCAGAA	2639
QY	4326	AAGCGGCCATTTTCCACCATGATTTTCGCGCAAGCGGCATCGCCATGGGTTCAGACGAG	4385
DB	2640	AAGCGGCCATTTTCCACCATGATTTTCGCGCAAGCGGCATCGCCATGGGTTCAGACGAG	2699
QY	4386	TCCTCCCGTTCGGGCATGCGCGCTTGGAGCTTGGCGAAACAGTTTCGGCTGCGCGAGCCCC	4445
DB	2700	TCCTCCCGTTCGGGCATGCGCGCTTGGAGCTTGGCGAAACAGTTTCGGCTGCGCGAGCCCC	2759
QY	4446	TGATGCTCTTCGTCAGATCATCTCATGACAAAGACCCGCTTCCATCCGAGTACGTGCT	4505
DB	2760	TGATGCTCTTCGTCAGATCATCTCATGACAAAGACCCGCTTCCATCCGAGTACGTGCT	2819
QY	4506	CGCTCATGCGATGTTTTCGCTTGGTGTGGAATGGGCGAGTAGCCGAGTCAAGCGTATGC	4565

Db 2072 GCTGGGCTGTGTCAGAAACCCCGCTTCAGCCCGACCGCTGCGCCTTATCCGGTAACCTA 2131
QY 3426 TCCTCTTGAGTCAACCCCGTAAGACACGACTTATCGCCATCGGCAGACCACTCGTAA 3485
Db 2132 TCCTCTTGAGTCAACCCCGTAAGACACGACTTATCGCCATCGGCAGACCACTCGTAA 2191
QY 3486 CAGGATTAGCAGACGAGTATAGCGGTGCTACAGAGTTCTTGAAGTGTGGCTAA 3545
Db 2192 CAGGATTAGCAGACGAGTATAGCGGTGCTACAGAGTTCTTGAAGTGTGGCTAA 2251
QY 3546 CTACGCTACACTAGAAAGACAGTATTTGGTATCTGCTCTCTGCTCAAGCCAGTATACCTT 3605
Db 2252 CTACGCTACACTAGAAAGACAGTATTTGGTATCTGCTCTCTGCTCAAGCCAGTATACCTT 2311
QY 3606 CGGAAAAGAGTTGGTAGCTCTTGTATCCGSCAAACAAACACCGCTGGTAGCGGTGTTTT 3665
Db 2312 CGGAAAAGAGTTGGTAGCTCTTGTATCCGSCAAACAAACACCGCTGGTAGCGGTGTTTT 2371
QY 3666 TTTTGTGTTGCAAGCAGAGATTACGGCAGAGAAAAAGGATCTCAAGAGATCCTTTGAT 3725
Db 2372 TTTTGTGTTGCAAGCAGAGATTACGGCAGAGAAAAAGGATCTCAAGAGATCCTTTGAT 2431
QY 3726 CTTTCTCTACGGGTCTGACGCTCAGTGGAACGAAACTCAGGTTAAGGGATTTTGTGCTAT 3785
Db 2432 CTTTTCTACGGGTCTGA ----- 2449
QY 3786 GAGATTATCGTGACCAAGCGCCATCGTGCCTCCCACTCTCGCAGTTTCGGGGGCATG 3845
Db 2450 ----- 2449
QY 3846 GATCGCGGATAGCGGTGCTGTTCTTGATGTCGACGGATTGCACTGCGCGTAGAA 3905
Db 2450 ----- 2449
QY 3906 CTCGCGAGTGTCTCAGCCTCAGGACGAGCTGAACCACTCGCGAGGGATCGAGCCC 3965
Db 2450 ----- 2449
QY 3966 GGGGTGGCGAAGAACTCCAGATGAGATCCCGCGCTGGAGGATCATCAGCCGCGTC 4025
Db 2450 ----- 2449
QY 4026 CCGGAAAACGATTCCGAGGCCCAACCTTTCATAGAGGGCGGCGTGAATCGAAATCTCG 4085
Db 2450 ----- 2449
QY 4086 TGATGGCAGGTTGGGCGTCTGTTGGTCTGTCATTTTCGAACCCAGAGTCCCGCTCAGAAG 4145
Db 2450 -----CGTCAAGAG 2459
QY 4146 AACTCGTCAAGAGCGGATAGAGGCGATCGCTGCGAATPCGGAGCGGCGATACCGTAA 4205
Db 2460 AACTCGTCAAGAGCGGATAGAGGCGATCGCTGCGAATCGGAGCGGCGATACCGTAA 2519
QY 4206 AGCAGGGAAGCGGTACGCCCATTCGCCCGAAGCTCTTCAGCAATATCACGGGTAGCC 4265
Db 2520 AGCAGGGAAGCGGTACGCCCATTCGCCCGAAGCTCTTCAGCAATATCACGGGTAGCC 2579
QY 4266 AACGCTATGCTCTGATAGCGGTCCGCCACACCGCGGCCACAGTCGATGAATTCAGAA 4325
Db 2580 AACGCTATGCTCTGATAGCGGTCCGCCACACCGCGGCCACAGTCGATGAATTCAGAA 2639
QY 4326 AAGCGGCCATTTTCCACATGATATTCGGAAGCAGGCATCGCCATGGGTCAACGACGAGA 4385
Db 2640 AAGCGGCCATTTTCCACATGATATTCGGAAGCAGGCATCGCCATGGGTCAACGACGAGA 2699
QY 4386 TCCTCGCCGTTCGGGCATCGCGCTTGAGCCTGGCGAAAGATTTCGGTGGCGGAGGCC 4445
Db 2700 TCCTCGCCGTTCGGGCATCGCGCTTGAGCCTGGCGAAAGATTTCGGTGGCGGAGGCC 2759
QY 4446 TGATGCTCTTCGTCCAGATCATCTGATCGACAGACCGGCTTCATCCGAGTACGTGCT 4505

Db 2760 TGATGCTCTTCGTCCAGATCATCTGTATCGAACAGCGGCTTCCATCCGAGTACGTGCT 2819
QY 4506 CGCTCGATCGCATGTTTTCGCTTGGTGTGCTGAATGGCAGGTAGCCGGATCAAGCGGTATGC 4565
Db 2820 CGCTCGATCGCATGTTTTCGCTTGGTGTGCTGAATGGCAGGTAGCCGGATCAAGCGGTATGC 2879
QY 4566 AGCCCGCATTTGCATTCAGCCATGAGTATCTTTCTCGGAGGAGCAAGGTGAGATGAC 4625
Db 2880 AGCCCGCATTTGCATTCAGCCATGAGTATCTTTCTCGGAGGAGCAAGGTGAGATGAC 2939
QY 4626 AGGAGATCTTCGCCCGGCACCTTCGCCCAATAGCAGCAGTCTCTCCCGCTTCAGTGACA 4685
Db 2940 AGGAGATCTTCGCCCGGCACCTTCGCCCAATAGCAGCAGTCTCTCCCGCTTCAGTGACA 2999
QY 4686 AGTGTAGACAGTGTGCGAAGAACGCCGCTGTGTGGCCAGCCACGATAGCCGCGTGC 4745
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QY 4746 TCGTCTCTCAGTTCATTTCAGGGCACCGGACAGTCTGTTCACAAAAAGAACCGGCGC 4805
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Db 3120 CCTGTGCTGTACAGCGCGAAACACGCGGCATCAGAGCAGCCGATTGTCTGTGTGCCAG 3179
QY 4866 TCATAGCCGAATAGCTCTTCACCCAGCGCGGAGAACCTTCGCTGCGAATCCATCTTGT 4925
Db 3180 TCATAGCCGAATAGCTCTTCACCCAGCGCGGAGAACCTTCGCTGCGAATCCATCTTGT 3239
QY 4926 TCAATCATCGAAACGATCTCTCTCTTGTATCAGATCTTCATCCCTGCGCCAT 4985
Db 3240 TCAATCATCGAAACGATCTCTCTCTTGTATCAGATCTTCATCCCTGCGCCAT 3299
QY 4986 CAGATCCTTTGGCGGCAAGAACCCATCCAGTTTACTTTTCAGGGCTTCCCAACCTTACCA 5045
Db 3300 CAGATCCTTTGGCGGCAAGAACCCATCCAGTTTACTTTTCAGGGCTTCCCAACCTTACCA 3359
QY 5046 GAGGGGCCCCAGCTGGCAATTCGGTTTCGTTGCTGTCTCATATAAACCGGCCAGTCTAGC 5105
Db 3360 GAGGGGCCCCAGCTGGCAATTCGGTTTCGTTGCTGTCTCATATAAACCGGCCAGTCTAGC 3419
QY 5106 TATCGCCATGTAAAGCCACTGCAAGCTACCTGCTTCTCTT 5146
Db 3420 AACTGTGGAAAGGCGCATCGGTGCGGCTCTCTGCTATT 3460

RESULT 15

AAL62059

ID AAL62059 standard; DNA; 3534 BP.

XX AAL62059;

XX AC

XX 22-SRP-2003 (first entry)

XX TI-GHRH plasmid DNA.

XX Plasmid-mediated supplementation; anaemia; tumour; adenoma; melanoma;

KW sarcoma; immune dysfunction; carcinoma; leukaemia; kidney failure;

KW lymphoma; weight loss; lymphopoesis; appetite stimulant; anorectic;

KW growth hormone releasing hormone; GHRH; cyclic; circular; gene; ds.

XX Unidentified.

OS WO2003049700-A2.

PN 19-JUN-2003.

XX 10-DEC-2002; 2002WO-US039509.

XX 11-DEC-2001; 2001US-0339610P.

XX (ADVI-) ADVISYS INC.

PA (BAYU) BAYLOR COLLEGE MEDICINE.
XX Dregbia-Akli R, Carpenter RH, Kern DR, Schwartz RJ, King G;
PI Hahn K, Brenner MK;
XX WPI; 2003-558968/52.
XX
PT Treating anemia, immune dysfunction, tumor, increasing total red blood
PT cell mass, reversing wasting or abnormal weight loss in subject, by
PT administering nucleic acid construct encoding growth-hormone-releasing-
PT hormone.
XX
XX Claim 4; Page 191-193; 212pp; English.
XX
XX The invention relates to compositions and methods for plasmid-mediated
XX supplementation. The method is useful for treating anaemia, tumour (such
XX as adenoma, mast cell tumour, melanoma, sarcoma or solid tumour), immune
XX dysfunction, carcinoma (benign or malignant), leukaemia, lymphoma or
XX kidney failure, for preventing the development of metastatic tumour, for
XX increasing total red blood cell mass, for reversing wasting, abnormal
XX weight loss or suppression of lymphopoiesis, in a subject, or for
XX increasing weight gain in a chronically ill subject or, or for extending
XX life expectancy for a chronically ill subject. The present sequence is TI
XX -growth hormone releasing hormone (GHRH) plasmid DNA. This sequence is
XX used to illustrate the method of the invention
XX
SQ Sequence 3534 BP; 764 A; 1017 C; 978 G; 775 T; 0 U; 0 Other;

Query Match 30.4%; Score 1603.8; DB 9; Length 3534;
Best Local Similarity 82.8%; Pred. No. 2.5e-234;
Matches 2022; Conservative 0; Mismatches 27; Indels 392; Gaps 1;

QY 2706 CTAGACCTAATCATGGTCATAGCTGTTCTCTGTGTGAATTTGTTATCCGGCTCACAATTC 2765
DB 1412 CTGGCGTAATCATGGTCATAGCTGTTCTCTGTGTGAATTTGTTATCCGCTCACAATTC 1471

QY 2766 ACAACAATAGAGCCGGAAGCAATAAGTGTAAAGCTGGGGTGCCTTAATGAGTGAGCTA 2825
DB 1472 ACAACAATAGAGCCGGAAGCAATAAGTGTAAAGCTGGGGTGCCTTAATGAGTGAGCTA 1531

QY 2826 ACTCACATTAATGGCTGGCTCAGTCCCGCTTTCAGTCGGGAACCTGTGTCGA 2885
DB 1532 ACTCACATTAATGGCTGGCTCAGTCCCGCTTTCAGTCGGGAACCTGTGTCGA 1591

QY 2886 GCTGCATTAATGAATCGGCCAAGCCGCGGAGAGCGGTTTGGTATTGGCGCTCTTC 2945
DB 1592 GCTGCATTAATGAATCGGCCAAGCCGCGGAGAGCGGTTTGGTATTGGCGCTCTTC 1651

QY 2946 CGTTCTCTCGCTCACTGACTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCT 3005
DB 1652 CGTTCTCTCGCTCACTGACTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGC 1711

QY 3006 TCACCTAAAGCCGTAATACGGTTATCCACAGATCAGGGATTAACCGAGGAAGACAT 3065
DB 1712 TCACCTAAAGCCGTAATACGGTTATCCACAGATCAGGGATTAACCGAGGAAGACAT 1771

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DB 1772 GTGAGCAAAAGGCCAGCAAAAGGCCAGAACCGTAAAGCCGCGTGTGCTGGGTTTTT 1831

QY 3126 CCATAGGCTCCGCCCTCGCTGACGAGCATCAAAAATCGACGCTCAAGTCAGAGGTGGCG 3185
DB 1832 CCATAGGCTCCGCCCTCGCTGACGAGCATCAAAAATCGACGCTCAAGTCAGAGGTGGCG 1891

QY 3186 AAACCCGACAGGACTATAAGATACAGGGGTTTTCCCTCTGGAAGCTCCCTCTGTGGCTC 3245
DB 1892 AAACCCGACAGGACTATAAGATACAGGGGTTTTCCCTCTGGAAGCTCCCTCTGTGGCTC 1951

QY 3246 TCCTGTTCCGACCTCGCGCTTACCGGATACCTGTGCGGCTTTCTCCCTTCGGGAGCGT 3305
DB 1952 TCCTGTTCCGACCTCGCGCTTACCGGATACCTGTGCGGCTTTCTCCCTTCGGGAGCGT 2011

QY 3306 GCGCGTTTCTCATAGCTCAAGCTGTAGGTATCTCAGTTCCGTTGAGTGTAGTGTGCTCAA 3365

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QY 3366 GCTGGGCTGTGTCAGCAACCCCGGTTACGCCGCGGCGGCTTATCCCGTAACTA 3425
DB 2072 GCTGGGCTGTGTCAGCAACCCCGGTTACGCCGCGGCGGCTTATCCCGTAACTA 2131
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DB 2132 TCCTGTTGAGTCAACCCCGGTAAGACACGACTTATTCGCCACTGCGCAGCAGCACTGGTAA 2191
QY 3486 CAGGATTAGCAGAGCGAGGTATGTAGCGGTGCTACAGAGTCTTTGAAGTGGTGGCTTAA 3545
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QY 3546 CTACGGCTACACTAGAGACAGTATTGTTGTTACTGCTCTGCTGCTGCTGCTGCTGCTGCT 3605
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QY 3606 CGGAAAAGAGTTGGTAGCTCTTTCATCCGGCAACCAACCAACCAACCAACCAACCAACCA 3665
DB 2312 CGGAAAAGAGTTGGTAGCTCTTTCATCCGGCAACCAACCAACCAACCAACCAACCAACCA 2371
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DB 2372 TTTTGTGTTCAAGCAGCAGATTACGGCAGAAAAAGGATCTCAAGAAAGATCTTTGAT 2431
QY 3726 CTCTTCTACGGGCTCTGACGCTCAGTGTGAACGAAACTCAGTTAAGGATTTTGGTCAT 3785
DB 2432 CTCTTCTACGGGCTCTGACGCTCAGTGTGAACGAAACTCAGTTAAGGATTTTGGTCAT 2449
QY 3786 GAGATTATCTGTCGACCAAGCGGCTCGTGTGCTCTCCCACTCTCTGAGTTCCGGGGCATG 3845
DB 2450 ----- 2449
QY 3846 GATGCGCGGATAGCCGCTGCTGTTTCTGATGTCGACGGAATTTGCACTGCCGGTAA 3905
DB 2450 ----- 2449
QY 3906 CTCCGCGAGTCTCGTCAGCTCAGGAGCAGCTGACCAACTCGGAGGGGATCGAGCCC 3965
DB 2450 ----- 2449
QY 3966 GGGGTGGCGAAGAACTCCAGCATGAGATCCCGCGCTGGAGGATCATCCAGCGCGGCTC 4025
DB 2450 ----- 2449
QY 4026 CCGGAAAAAGATTCCGAAGCCCAACTTTTCATAGAGGCGCGGTGGAATTCGAAATCTCG 4085
DB 2450 ----- 2449
QY 4086 TGATGGCAGGTTGGGCGTCTGTTGGTCTGCTATTCGAAACCCAGAGTCCGCTCAGAA 4145
DB 2450 ----- 2459
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DB 2520 AGCAGGAGGAGCGGTGAGCCCAATTCGCGCCCAAGCTCTTCAGCAATATCACGGGTAGCC 2579
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Qy 4566 AGCGCGCGCATTCGATCAGCATGATGGATACCTTCTCGGACAGGAGCAAGGTGAGATGAC 4625
Db 2880 AGCGCGCGCATTCGATCAGCATGATGGATACCTTCTCGGACAGGAGCAAGGTGAGATGAC 2939
Qy 4626 AGGAGATCCCTGCCCCGGGACTTCGCCCAATAGCAGCGAGTCCCTTCCCGTTTCAGTGACA 4685
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Qy 4686 ACCTCGAGCACAGCTCGCAAGGAACGCCGTCGTGGCCAGCCACGATAGCCGCGCTGCC 4745
Db 3000 ACCTCGAGCACAGCTCGCAAGGAACGCCGTCGTGGCCAGCCACGATAGCCGCGCTGCC 3059
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Qy 5046 GAGGGCGCCCGAGTGGCAATTCGGTTTCGGTTTCCTGTCATAAACCGCCAGTCTAGC 5105
Db 3360 GAGGGCGCCCGAGTGGCAATTCGGTTTCGGTTTCCTGTCATAAACCGCCAGTCTAGC 3419
Qy 5106 TATCGCCCATGTAAAGCCCACTGCAAGCTACCTGCTTTCTTT 5146
Db 3420 AACTGTTGGGAAGGGGATCGGTGCGGGCTCTTCGCTATT 3460

Search completed: July 3, 2005, 08:35:12
Job time : 2636 secs

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OM nucleic - nucleic search, using sw model

Run on: July 2, 2005, 20:36:53 ; Search time 792 Seconds
(without alignments)
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Title: US-09-921-143-36

Perfect score: 5283

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Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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6: /cgn2_6/ptodata/1/ina/backfiles.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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C 2	1793.4	33.9	4800	4	US-09-584-329-1
C 3	1652.4	31.3	5594	3	US-09-380-190A-29
C 4	1618.2	30.6	6561	3	US-09-380-190A-30
C 5	1602.2	30.3	5707	2	US-08-472-809B-8
C 6	1571.6	29.7	4665	3	US-08-948-378A-7
C 7	1571.6	29.7	4665	3	US-09-169-425C-7
C 8	1571.6	29.7	4665	4	US-09-759-960-7
C 9	1570	29.7	4518	3	US-09-380-190A-26
C 10	1570	29.7	4886	3	US-09-533-220A-4
C 11	1570	29.7	6139	2	US-08-751-767A-7
C 12	1569.8	29.7	4748	4	US-09-796-575-4
C 13	1569.8	29.7	4992	4	US-09-796-575-5
C 14	1569.8	29.7	5069	4	US-09-393-483A-1
C 15	1569.8	29.7	5069	4	US-09-393-483A-2
C 16	1569.8	29.7	8797	2	US-08-723-306-6
C 17	1569.8	29.7	8797	5	PCT-US96-10041-6
C 18	1569.8	29.7	11093	2	US-08-723-306-5
C 19	1569.8	29.7	11093	5	PCT-US96-10041-5
C 20	1564.2	29.6	5532	4	US-08-961-888-40
C 21	1501.4	28.4	6795	3	US-09-380-190A-22
C 22	1501.4	28.4	8574	4	US-09-554-572-3
C 23	1501.4	28.4	9093	3	US-09-380-190A-23
C 24	1501.4	28.4	9093	4	US-09-554-572-2
C 25	1501.4	28.4	9145	4	US-09-554-572-1
C 26	1501	28.4	4958	3	US-09-380-190A-20
C 27	1501	28.4	5754	3	US-09-380-190A-18

C 28	1501	28.4	5754	3	US-09-380-190A-19
C 29	1501	28.4	6225	3	US-09-380-190A-1
C 30	1501	28.4	6321	3	US-09-380-190A-17
C 31	1501	28.4	6359	3	US-09-380-190A-15
C 32	1501	28.4	6891	3	US-09-380-190A-16
C 33	1501	28.4	8657	3	US-09-380-190A-14
C 34	1490.4	28.2	3974	3	US-09-026-343-33
C 35	1490.4	28.2	3974	3	US-09-042-105-16
C 36	1490.4	28.2	3974	3	US-09-044-856A-7
C 37	1490.4	28.2	3974	3	US-09-023-082A-147
C 38	1490.4	28.2	3974	3	US-09-044-855A-7
C 39	1490.4	28.2	3974	3	US-09-078-670-4
C 40	1490.4	28.2	3974	3	US-09-026-408-14
C 41	1490.4	28.2	3974	3	US-09-362-871-33
C 42	1490.4	28.2	3974	3	US-09-627-154-4
C 43	1490.4	28.2	3974	4	US-09-027-287-50
C 44	1490.4	28.2	3974	4	US-09-437-602-4
C 45	1490.4	28.2	3974	4	US-09-252-656B-50

ALIGNMENTS

RESULT 1

US-09-186-002-16

; Sequence 16, Application US/09186002B

; Patent No. 6489542

; GENERAL INFORMATION:

; APPLICANT: Corbin, David R.

; APPLICANT: Romano, Charles P.

; TITLE OF INVENTION: Improved Method for Transforming Plants to Express

; FILE REFERENCE: 38-21(13547) US Pat No. 6489542 09/186,002

; CURRENT APPLICATION NUMBER: US/09/186,002B

; CURRENT FILING DATE: 1998-11-04

; NUMBER OF SEQ ID NOS: 18

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 16

; LENGTH: 8349

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; NAME/KEY: gene

; LOCATION: (3666)..(5573)

; OTHER INFORMATION: completely synthesized

US-09-186-002-16

Query Match	42.4%	Score 2240;	DB 4;	Length 8349;
Best Local Similarity	93.4%	Pred. No. 0;		
Matches 2409;	Conservative	0;	Mismatches 25;	Indels 144;
Gaps	1;			
QY	2706	CTAGACGTAATCATGCTAGCTGTTCTCTGTGTAATTTGTTATCCGCTCAATTC	2765	
Db	5911	CTTGGCGTAATCATGCTAGCTGTTCTCTGTGTAATTTGTTATCCGCTCAATTC	5970	
QY	2766	ACACACATACGACGCGGAGCATAAAGTGAAGCTCGGGTGCCCTAATGAGTGACCTA	2825	
Db	5971	ACACACATACGACGCGGAGCATAAAGTGAAGCTCGGGTGCCCTAATGAGTGACCTA	6030	
QY	2826	ACTCACATTAATTCGTTGCGCTCACTGCGCGCTTTCCAGTCGCGGAAACCTGTCGTGCCA	2885	
Db	6031	ACTCACATTAATTCGTTGCGCTCACTGCGCGCTTTCCAGTCGCGGAAACCTGTCGTGCCA	6090	
QY	2886	GCTGCATTAATGAATCGGCCAACGCGGGGAGAGGGGTTTCGGTATTGGGCGCTTTC	2945	
Db	6091	GCTGCATTAATGAATCGGCCAACGCGGGGAGAGGGGTTTCGGTATTGGGCGCTTTC	6150	
QY	2946	CGCTTCTCGCTCACTGACTCGCTGCGCTGCGTTCGCTGCGCGGAGCGGTATCAGC	3005	
Db	6151	CGCTTCTCGCTCACTGACTCGCTGCGCTGCGTTCGCTGCGCGGAGCGGTATCAGC	6210	
QY	3006	TCACCTAAAGCGCGGTAAATACGGTTATCCACAGAAATCAGGGGATACCGAGGAAGACAT	3065	

Db 6211 TCACTCAAAGCGGTAAATACGGTTATCCACAGAAATCAGGGGATAACCGCAGGAAGAACAT 6270
QY 3066 GTGAGCAAAAGGCCAGCAAGAACCCGTAAAAAGGCGCGTGTGCTGCGCTTTT 3125
Db 6271 GTGAGCAAAAGGCCAGCAAGAACCCGTAAAAAGGCGCGTGTGCTGCGCTTTT 6330
QY 3126 CCATAGGCTCCGCCCGCTGACGAGCATCAAAAATCAGACGCTCAAGTCAGAGGTGGCG 3185
Db 6331 CCATAGGCTCCGCCCGCTGACGAGCATCAAAAATCAGACGCTCAAGTCAGAGGTGGCG 6390
QY 3186 AAACCCGACAGGACTATAAGATACCAAGCGTTTCCCTCTGGAAGCTCCCTGCTGCGCTC 3245
Db 6391 AAACCCGACAGGACTATAAGATACCAAGCGTTTCCCTCTGGAAGCTCCCTGCTGCGCTC 6450
QY 3246 TCCTGTTCCGACCGCTGCGCTTACCGGATACCTGTCCGCGCTTTCTCCCTTCGGGAAGCGT 3305
Db 6451 TCCTGTTCCGACCGCTGCGCTTACCGGATACCTGTCCGCGCTTTCTCCCTTCGGGAAGCGT 6510
QY 3306 GCGCGCTTCTCATAGCTCAGCTGTAGGTATCTCAGTTCCGTTAGGTGCTTCGCTCCAA 3365
Db 6511 GCGCGCTTCTCAATGCTCAGCTGTAGGTATCTCAGTTCCGTTAGGTGCTTCGCTCCAA 6570
QY 3366 GCTGGGCTGTGTCAGCAACCCCGTTACGCCGACCGCTGCGCTTATCCGCTTAATCCGCTAACTA 3425
Db 6571 GCTGGGCTGTGTCAGCAACCCCGTTACGCCGACCGCTGCGCTTATCCGCTTAATCCGCTAACTA 6630
QY 3426 TCCTGTTAGTCCAAACCCCGTTAAGACACGACTTATCGCCACTGGCAGCACTCGGTAA 3485
Db 6631 TCCTGTTAGTCCAAACCCCGTTAAGACACGACTTATCGCCACTGGCAGCACTCGGTAA 6690
QY 3486 CAGGATTAGCAGACGAGGTATGAGCGGTGCTACAGATTCTTGAAGTGTGGCTTAA 3545
Db 6691 CAGGATTAGCAGACGAGGTATGAGCGGTGCTACAGATTCTTGAAGTGTGGCTTAA 6750
QY 3546 CTACGGCTACACTAGAAAGACAGTATTGTTGTAATCTGCGCTCTGCTGAAGCCAGTTACCTT 3605
Db 6751 CTACGGCTACACTAGAAAGACAGTATTGTTGTAATCTGCGCTCTGCTGAAGCCAGTTACCTT 6810
QY 3606 CGGAAAAGAGTTGGTAGCTTCTGATCCGGCAAAACCAACCGCTGGTAGCGGTGGTTT 3665
Db 6811 CGGAAAAGAGTTGGTAGCTTCTGATCCGGCAAAACCAACCGCTGGTAGCGGTGGTTT 6870
QY 3666 TTTTGTCTGACGACGAGATTAGCGCGAAGAAAAGATCTCAAGAGATCCTTTGAT 3725
Db 6871 TTTTGTCTGACGACGAGATTAGCGCGAAGAAAAGATCTCAAGAGATCCTTTGAT 6930
QY 3726 CTTTCTTACGGGCTCTGACGCTCAGTGGAAACGAAACTCACGTTTAAGGGATTTTGTTCAT 3785
Db 6931 CTTTCTTACGGGCTCTGACGCTCAGTGGAAACGAAACTCACGTTTAAGGGATTTTGTTCAT 6990
QY 3786 GAGATTATCGTCGACCAAGCGGCGCATCGTGCCTCCCACTCCTGCAAGTTTCGGGGGCGATG 3845
Db 6991 GAGATTATCAAAAGGATCTTCACTAGATCCTT----- 7024
QY 3846 GATGCGCGGATAGCCGCTGCTGGTTTCTCGATGCGGACGGATTTGCACTGCGCGGTAGAA 3905
Db 7025 ----- 7024
QY 3906 CTCGCGAGGTCTGTCAGCCTCAGGACAGCTGAACCAACTCGCGAGGGGATCGAGCCC 3965
Db 7025 -----TT 7026
QY 3966 GGGGTGGCGAAGAACTCCAGCATGATATCCCGCGTGGAGGATCATCAGCCGCGCTC 4025
Db 7027 GGGGTGGCGAAGAACTCCAGCATGATATCCCGCGTGGAGGATCATCAGCCGCGCTC 7086
QY 4026 CCGGAAAACGATTCCGAGCCCACTTTTATAGAGGGCGGCGGTGGAATCGAAATCTCG 4085
Db 7087 CCGGAAAACGATTCCGAGCCCACTTTTATAGAGGGCGGCGGTGGAATCGAAATCTCG 7146
QY 4086 TGATGGCAGGTGGGGCTGCTGGTGGTCAATTTTCAACCCAGAGTCCCGCTCAGAAAG 4145
Db 7147 TGATGGCAGGTGGGGCTGCTGGTGGTCAATTTTCAACCCAGAGTCCCGCTCAGAAAG 7206

QY 4146 AACTCGTCAAGAAAGCGGATAGAAAGCGGATGCGCTCGGAATCGGAGCGCGATACCGTTAA 4205
Db 7207 AACTCGTCAAGAAAGCGGATAGAAAGCGGATGCGCTCGGAATCGGAGCGCGATACCGTTAA 7266
QY 4206 ASCACGAGAAAGCGGTACGCCCATTCGCCGCCAAGCTCTTCAGCAATATACAGGGTAGCC 4265
Db 7267 AGCACGAGAAAGCGGTACGCCCATTCGCCGCCAAGCTCTTCAGCAATATACAGGGTAGCC 7326
QY 4266 AACCGCTATCTCTGATAGCGGTCCGCCACACCCAGCGCGCCACAGTCGATGATATCAGAA 4325
Db 7327 AACCGCTATCTCTGATAGCGGTCCGCCACACCCAGCGCGCCACAGTCGATGATATCAGAA 7386
QY 4326 AAGCGCGCAATTTTCCACATGATATTCGGCAAGCAGGCAATCGCCATGGGTACGACGAGA 4385
Db 7387 AAGCGCGCAATTTTCCACATGATATTCGGCAAGCAGGCAATCGCCATGGGTACGACGAGA 7446
QY 4386 TCCTCGCGCTCGGGCATGCGCGCTTACGCTGGCGAAGCAGTTCCGCTGCGCGAGCCCC 4445
Db 7447 TCCTCGCGCTCGGGCATGCGCGCTTACGCTGGCGAAGCAGTTCCGCTGCGCGAGCCCC 7506
QY 4446 TGATGCTCTTTCGTCCAGATCATCTGATCGAACAAGACCCGCTTCCATCCGAGTACGTGCT 4505
Db 7507 TGATGCTCTTTCGTCCAGATCATCTGATCGAACAAGACCCGCTTCCATCCGAGTACGTGCT 7566
QY 4506 CGCTCGATCGGATGTTTTCGTGGTGGTGCATGGGCAAGTACGCGGATCAAGCGGTATGC 4565
Db 7567 CGCTCGATCGGATGTTTTCGTGGTGGTGCATGGGCAAGTACGCGGATCAAGCGGTATGC 7626
QY 4566 AGCGCGCATTTGCAATCAGCCATGATGATATCTTCTCGGAGGAGCAAGTGGATGAC 4625
Db 7627 AGCGCGCATTTGCAATCAGCCATGATGATATCTTCTCGGAGGAGCAAGTGGATGAC 7686
QY 4626 AGGAGATCTGCTCGCGGCACTTCGCGCCAAATAGCAGCCAGTCCCTTCCCGCTTCAGTGACA 4685
Db 7687 AGGAGATCTGCTCGCGGCACTTCGCGCCAAATAGCAGCCAGTCCCTTCCCGCTTCAGTGACA 7746
QY 4686 AGTTCAGACACAGCTGCGCAAGAACCGCGCTGCTGGCGCAGCAAGATAGCGCGCTGCC 4745
Db 7747 AGTTCAGACACAGCTGCGCAAGAACCGCGCTGCTGGCGCAGCAAGATAGCGCGCTGCC 7806
QY 4746 TCGTCTCGCAGTTCATTACAGGCGCACCGGACAGCTGCTTGACAAAAAGAACCGGCGC 4805
Db 7807 TCGTCTCGCAGTTCATTACAGGCGCACCGGACAGCTGCTTGACAAAAAGAACCGGCGC 7866
QY 4806 CCGTCGCTGACAGCGCGGAACACGCGGCATCAGAGCAGCCGATGCTGTTGTGCCAG 4865
Db 7867 CCGTCGCTGACAGCGCGGAACACGCGGCATCAGAGCAGCCGATGCTGTTGTGCCAG 7926
QY 4866 TCATAGCCGAATAGCCTCTCCACCAAGCGCGGAGAACCTGCGGTGCAATCCATCTTGT 4925
Db 7927 TCATAGCCGAATAGCCTCTCCACCAAGCGCGGAGAACCTGCGGTGCAATCCATCTTGT 7986
QY 4926 TCAATCATCGGAAACGATCCTGCTCTCTGATCAGATCTGATCCCTGCGCCAT 4985
Db 7987 TCAATCATCGGAAACGATCCTGCTCTCTGATCAGATCTGATCCCTGCGCCAT 8046
QY 4986 CAGATCCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTTCAGGGCTTCCCAACTTACCA 5045
Db 8047 CAGATCCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTTCAGGGCTTCCCAACTTACCA 8106
QY 5046 GAGGGCGCCCGAGCTGGCAATTCGGTTGCTGCTGCTGCTCAATAAAACCGCCGATGCTAGC 5105
Db 8107 GAGGGCGCCCGAGCTGGCAATTCGGTTGCTGCTGCTGCTCAATAAAACCGCCGATGCTAGC 8166
QY 5106 TATCGCCATGTAAGCCCACTGCAAGCTACCTGCTTCTCTTTGCGCTTGGTTTCCCTT 5165
Db 8167 TATCGCCATGTAAGCCCACTGCAAGCTACCTGCTTCTCTTTGCGCTTGGTTTCCCTT 8226
QY 5166 GTCCAGATGCCCGAGTACGATCATTCAGGGGTACAGCCGTTTCTGCGACATGGCT 5225
Db 8227 GTCCAGATGCCCGAGTACGATCATTCAGGGGTACAGCCGTTTCTGCGACATGGCT 8286

QY 5226 TTCTACGTTGTCCTTCTAGCAGCCCTTGGCCCTCAGTGTCTGCGCAGCGTG 5283
Db 8287 TTCTACGTTGTCCTTCTAGCAGCCCTTGGCCCTCAGTGTCTGCGCAGCGTG 8344

RESULT 2

US-09-554-929-1/c

; Sequence 1, Application US/09554929

; Patent No. 6521427

; GENERAL INFORMATION:

; APPLICANT: Evans, Glen A.

; TITLE OF INVENTION: A Method for the Complete Chemical

; TITLE OF INVENTION: Synthesis and Assembly of Genes and Genomes

; FILE REFERENCE: P-EA 4749

; CURRENT APPLICATION NUMBER: US/09/554.929

; CURRENT FILING DATE: 2000-05-12

; NUMBER OF SEQ ID NOS: 193

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 1

; LENGTH: 4800

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Synthetic plasmid

US-09-554-929-1

Query Match 33.9%; Score 1793.4; DB 4; Length 4800;
Best Local Similarity 91.8%; Pred. No. 0;
Matches 1980; Conservative 0; Mismatches 1; Indels 176; Gaps 1;

QY 3127 CATAGGCTCGCCCCCTGACGAGCATCAAAAAATCGACGCTCAAGTCTAGAGGTGGCGA 3186
Db 4800 CATAGGCTCGCCCCCTGACGAGCATCAAAAAATCGACGCTCAAGTCTAGAGGTGGCGA 4741

QY 3187 AACCCGACGAGACTATAAGATACAGCGGTTCCCTCGAAGCTCCCTCGCTCT 3246
Db 4740 AACCCGACGAGACTATAAGATACAGCGGTTCCCTCGAAGCTCCCTCGCTCT 4681

QY 3247 CCTGTTCCGACCTCGCGCTTACCGGATACCTGTCGCTTCTCCCTTCGGGAAGCGTG 3306
Db 4680 CCTGTTCCGACCTCGCGCTTACCGGATACCTGTCGCTTCTCCCTTCGGGAAGCGTG 4621

QY 3307 GCGCTTCTCATAGCTCAGCTGATGATCTCAGTTGCGTGTAGTGTGCTTCCGCTCAAG 3366
Db 4620 GCGCTTCTCATAGCTCAGCTGATGATCTCAGTTGCGTGTAGTGTGCTTCCGCTCAAG 4561

QY 3367 CTGGCTGTGTGACGAAACCCCGTTGACGCCGACCGCTGCGCTTATCGGTAACTAT 3426
Db 4560 CTGGCTGTGTGACGAAACCCCGTTGACGCCGACCGCTGCGCTTATCGGTAACTAT 4501

QY 3427 CGTCTTGAGTCCAAACCCGTAAGACACGACTTATCGCCTATGCGCAGCAGCCACTGGTAAC 3486
Db 4500 CGTCTTGAGTCCAAACCCGTAAGACACGACTTATCGCCTATGCGCAGCAGCCACTGGTAAC 4441

QY 3487 AGGATTAGCAGAGCGAGTATGTAAGCGGTGCTACAGAGTCTTTGAAGTGTGTCCTTAAC 3546
Db 4440 AGGATTAGCAGAGCGAGTATGTAAGCGGTGCTACAGAGTCTTTGAAGTGTGTCCTTAAC 4381

QY 3547 TAGCGCTACACTAGAGAAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTACCTTC 3606
Db 4380 TAGCGCTACACTAGAGAAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTACCTTC 4321

QY 3607 GGAAGAAAGAGTTGGTAGCTCTTGATCCGGCAAAACAAACCCAGCTGTGTAGCGGTGTTTT 3666
Db 4320 GGAAGAAAGAGTTGGTAGCTCTTGATCCGGCAAAACAAACCCAGCTGTGTAGCGGTGTTTT 4261

QY 3667 TTTGTTTTCAGCAGCAGATTAACCGCAGAAAAAAGGATCTCAAGAGATCTCTTTGATC 3726
Db 4260 TTTGTTTTCAGCAGCAGATTAACCGCAGAAAAAAGGATCTCAAGAGATCTCTTTGATC 4201

QY 3727 TTTTCTACGGGCTCAGCGCTCAGTGGAAACGAAACCTCAGTTAAGGATTTTGGTCATG 3786
Db 4200 TTTTCTACGGGCTCAGCGCTCAGTGGAAACGAAACCTCAGTTAAGGATTTTGGTCAT - 4142

QY 3787 AGATTATCGTCGAAAGCGGCATCGTGTCTCCCACTCTCTGAGTTCTGGGCGCATGG 3846
Db 4141 ----- 4142

QY 3847 ATGCGCGGATAGCGCTGTGCTTCTGAGTCCGACCGATTTGCACTGCGCGGTAGAAC 3906
Db 4141 ----- 4142

QY 3907 TCCGCGAGGTGCTCCAGCCTCAGGCAGCAGCTGAACCACTCGCGAGGGGATCGAGCCG 3966
Db 4141 -----GCGCG 4137

QY 3967 GGGTGGCGGAAGAACTCCAGCATGAGATCCCGCGCTGGAGGATCATCCAGCCGCGCTCC 4026
Db 4136 GGGTGGCGGAAGAACTCCAGCATGAGATCCCGCGCTGGAGGATCATCCAGCCGCGCTCC 4077

QY 4027 CGGAAACGATTTCCGAAGCCCAACCTTTTATAGAGCGCGGTGGAATCGAAATCTCGT 4086
Db 4076 CGGAAACGATTTCCGAAGCCCAACCTTTTATAGAGCGCGGTGGAATCGAAATCTCGT 4017

QY 4087 GATGGCAGGTTGGCGCTCGCTTCGATTCGAAACCCAGAGTCCCGCTCAGAGA 4146
Db 4016 GATGGCAGGTTGGCGCTCGCTTCGATTCGAAACCCAGAGTCCCGCTCAGAGA 3957

QY 4147 ACTCGTCAAGAGCGGATAGAGCGGATGCGCTGCGAATCGGAGCGCGCATACCGTAAA 4206
Db 3956 ACTCGTCAAGAGCGGATAGAGCGGATGCGCTGCGAATCGGAGCGCGCATACCGTAAA 3897

QY 4207 GCAAGAGAGCGGTTCAGCCCATTCGCGCCCAAGCTTTTCAGCAATATCAGGGTAGCCA 4266
Db 3896 GCAAGAGAGCGGTTCAGCCCATTCGCGCCCAAGCTTTTCAGCAATATCAGGGTAGCCA 3837

QY 4267 ACCTATGCTCTCATAGCGGTTCGCCACACCCAGCGGCCACAGTTCGATGAATCCAGAA 4326
Db 3836 ACCTATGCTCTCATAGCGGTTCGCCACACCCAGCGGCCACAGTTCGATGAATCCAGAA 3777

QY 4327 AGCGGCAATTTTCCACCATGATATTCGGCAAGCAGGATCGCATGCGGTCAACACGAGAT 4386
Db 3776 AGCGGCAATTTTCCACCATGATATTCGGCAAGCAGGATCGCATGCGGTCAACACGAGAT 3717

QY 4387 CTTGCGCGTTCGGCATTCGCGCTTCGAGCTGCGCAACAGTTTCGGTTCGCGCGAGCCCT 4446
Db 3716 CTTGCGCGTTCGGCATTCGCGCTTCGAGCTGCGCAACAGTTTCGGTTCGCGCGAGCCCT 3657

QY 4447 GATGCTCTTCGTCAGATCATCTGATCGACAGACCGGCTTCATCCGAGTACGTGCTC 4506
Db 3656 GATGCTCTTCGTCAGATCATCTGATCGACAGACCGGCTTCATCCGAGTACGTGCTC 3597

QY 4507 GCTCGATGCGATGTTTCGCTTGGTTCGAAATGGCGAGGTAGCGCGATCAAGCGTATGCA 4566
Db 3596 GCTCGATGCGATGTTTCGCTTGGTTCGAAATGGCGAGGTAGCGCGATCAAGCGTATGCA 3537

QY 4567 GCGCGCGCATTCGATCAGCCATGATGATATTTTCGCGAGGAGCAAGGTGAGATGACA 4626
Db 3536 GCGCGCGCATTCGATCAGCCATGATGATATTTTCGCGAGGAGCAAGGTGAGATGACA 3477

QY 4627 GGAGATCTTCGCGCGCATTCGCGCAATAGCAGCCAGTCCCTTCGCGCTTCAGTGACAA 4686
Db 3476 GGAGATCTTCGCGCGCATTCGCGCAATAGCAGCCAGTCCCTTCGCGCTTCAGTGACAA 3417

QY 4687 CGTTCGAGCAGCTGCGCAAGGAAACCGCGTTCGTCGCGCAGCCACGATAGCCGCGCTGCT 4746
Db 3416 CGTTCGAGCAGCTGCGCAAGGAAACCGCGTTCGTCGCGCAGCCACGATAGCCGCGCTGCT 3357

QY 4747 CGTCTTCGAGTTCATTCAGGGCACCGGACAGGTTCGCTTCGCAAAAAGAACCGCGCGCC 4806
Db 3356 CGTCTTCGAGTTCATTCAGGGCACCGGACAGGTTCGCTTCGCAAAAAGAACCGCGCGCC 3297

QY 4807 CTTGCGCTGACAGCCGGAACAAGCGCGCATCAGAGCAGCGGATTCGCTGTTGCGCCAGT 4866
Db 3296 CTTGCGCTGACAGCCGGAACAAGCGCGCATCAGAGCAGCGGATTCGCTGTTGCGCCAGT 3237

4867 CATAGCGAATAGCTCTCCACCAAGCGCGGAGAACTGGTGCAATCCATCTTGTT 4926
3236 CATAGCGAATAGCTCTCCACCAAGCGCGGAGAACTGGTGCAATCCATCTTGTT 3177
4927 CAATCATGCGAAGAGATCCTCATCTCTCTTTGATCAGATCTTGATCCCTCGGCCATC 4986
3176 CAATCATGCGAAGAGATCCTCATCTCTCTTTGATCAGATCTTGATCCCTCGGCCATC 3117
4987 AGATCTTGGCGGAGAGAAAGCCATCCAGTTTACTTTGAGGGCTTCCCAACCTTACCAG 5046
3116 AGATCTTGGCGGAGAGAAAGCCATCCAGTTTACTTTGAGGGCTTCCCAACCTTACCAG 3057
5047 AGGCGGCCAGCTGGCAATTCGGTTTCGCTGTCATTAACAAACCGCCAGCTAGCT 5106
3056 AGGCGGCCAGCTGGCAATTCGGTTTCGCTGTCATTAACAAACCGCCAGCTAGCT 2997
5107 ATGCCATGTAAGCCCACTGCAAGCTACCTGCTTTCTTTTGGCGTTTGGCTTTCCCTTG 5166
2996 ATGCCATGTAAGCCCACTGCAAGCTACCTGCTTTCTTTTGGCGTTTGGCTTTCCCTTG 2937
5167 TCAGATAGCCCAAGTACATGATTCATCCGGGGTACGACCCGTTTTCGCGACTGGCTT 5226
2936 TCAGATAGCCCAAGTACATGATTCATCCGGGGTACGACCCGTTTTCGCGACTGGCTT 2877
5227 TCTACGTGTTCCGCTTCTTTAGCAGCCCTTGGCCCTGAGTCTTGGCGCAGCGTG 5283
2876 TCTACGTGTTCCGCTTCTTTAGCAGCCCTTGGCCCTGAGTCTTGGCGCAGCGTG 2820

RESULT 3

US-09-380-190A-29/c
; Sequence 29, Application US/09380190A
; Patent No. 6410220
; GENERAL INFORMATION:
; APPLICANT: NATURE TECHNOLOGY CORPORATION, ET AL.
; TITLE OF INVENTION: SELF-ASSEMBLING GENES, VECTORS AND USES
; THEREOF
; NUMBER OF SEQUENCES: 74
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MUETING, RAASCH & GEBHARDT, P.A.
; STREET: 119 NORTH FOURTH STREET, SUITE 203
; CITY: MINNEAPOLIS
; STATE: MINNESOTA
; COUNTRY: USA
; ZIP: 55401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/380,190A
; FILING DATE: 26-Aug-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US98/03918
; FILING DATE: 28-FEB-98
; ATTORNEY/AGENT INFORMATION:
; NAME: MUETING, ANN M.
; REGISTRATION NUMBER: 33,977
; REFERENCE/DOCKET NUMBER: 228.00010201
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-305-1217
; TELEFAX: 612-305-1228
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5594 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 29:
US-09-380-190A-29

Query Match 31.3%; Score 1652.4; DB 3; Length 5594;
Best Local Similarity 85.4%; Pred. No. 0; Mismatches 261; Indels 67; Gaps 4;
Matches 1916; Conservative 0;
QY 3107 CGCGGTGCTGGCGTTTTTCCATAGGCTCCGCCCTCGAGCATCAAAAATCGAC 3166
DB 5591 CGCGGTGCTGGCGTTTTTCCATAGGCTCCGCCCTCGAGCATCAAAAATCGAC 5532
QY 3167 GCTCAAGTCAGAGTGGCGAAACCCGAGCAGGACTATAAGATACAGGGCTTCCCGCTG 3226
DB 5531 GCTCAAGTCAGAGTGGCGAAACCCGAGCAGGACTATAAGATACAGGGCTTCCCGCTG 5472
QY 3227 GAAGCTCCCTCGTGGCGTCTCTCTTCCGACCCCTCGGATACCTTGTCCGCT 3286
DB 5471 GAAGCTCCCTCGTGGCGTCTCTCTTCCGACCCCTCGGATACCTTGTCCGCT 5412
QY 3287 TTCTCCCTTCGGGAAGCGTGGCGCTTTTCTCATAGCTCAGCTGTAGGTATCTCAGTTCCG 3346
DB 5411 TTCTCCCTTCGGGAAGCGTGGCGCTTTTCTCATAGCTCAGCTGTAGGTATCTCAGTTCCG 5352
QY 3347 TGTAGTTCGTTCCGCTCAAGCTGGGCTGTGTGCAAGAACCCCGCTTCAGCCCGACCGCT 3406
DB 5351 TGTAGTTCGTTCCGCTCAAGCTGGGCTGTGTGCAAGAACCCCGCTTCAGCCCGACCGCT 5292
QY 3407 GCGCCTTATCCGCTAACCTATCTTGTAGTCCAAACCCGTAAGACACAGCTTATCGCCAC 3466
DB 5291 GCGCCTTATCCGCTAACCTATCTTGTAGTCCAAACCCGTAAGACACAGCTTATCGCCAC 5232
QY 3467 TGGCAGCAGCCACTGGTAAACAGGATTTAGCAGCAGGATTTAGCGGTGCTACAGAGT 3526
DB 5231 TGGCAGCAGCCACTGGTAAACAGGATTTAGCAGCAGGATTTAGCGGTGCTACAGAGT 5172
QY 3527 TCTTGAAGTGGTGGCTAACTACGCGTACACTAGAAGAACAGTATTTGGTATCTCGGCTC 3586
DB 5171 TCTTGAAGTGGTGGCTAACTACGCGTACACTAGAAGAACAGTATTTGGTATCTCGGCTC 5112
QY 3587 TGCTGAAGCCAGTTACCTTCGGAAAGAGTGGTAGCTCTTGATCCGCGCAACAAACCA 3646
DB 5111 TGCTGAAGCCAGTTACCTTCGGAAAGAGTGGTAGCTCTTGATCCGCGCAACAAACCA 5052
QY 3647 CGCTGCTAGCGTGGTTTTTTTGTGCAAGCAGCAGATTTAGCGCGCAGAAAAAAGGAT 3706
DB 5051 CGCTGCTAGCGTGGTTTTTTTGTGCAAGCAGCAGATTTAGCGCGCGCCGAGTGAGG 4992
QY 3707 CTCAGGAAGATCTTTTGTATCTTCTAAGGGTCTGACGCTC-----AGTGAACG 3757
DB 4991 GGTGTGGGCTCTTTTATTGAGCTCGGGGAGCAGAAAGCGCGCAACAGAAAGCAGAAAGCG 4932
QY 3758 AAAAATCAGGTTAAGGGATTTTGGTCATGAGATTTATCGTCAACAAAGCGCCATCGTGC 3817
DB 4931 AACTGATGGTTAGTTCAAAATAGGCACAGGGTCACTTTCAGGTCTTGGGGCACCTGGA 4872
QY 3818 CTC-----CCCACTCTCTGAGTTTGGGGGCGATGATGCGCGGATAGCGCGCTG 3864
DB 4871 AACATCTGATGGTTCTCTAGAAACTGCTGAGGGCTGACCGCATCTGGGGACCATCTGTT 4812
QY 3865 CTGGTTTCTTGAATCCGACCGGATTTGC-----ACTGCGGTAGAACTCCCGGAG 3914
DB 4811 CTGGGGCTTGAAGCGGGGCGAGAACTGCTTACACAGATATCTCTTGGGCCATATTCA 4752
QY 3915 GTGCTCAGCCTCAGGCAGCAGCTGAACCAACTCGGAGGGGATCGAGCCGGGTGGGC 3974
DB 4751 GCTGTTCCATCTGTTCTTGGCCCTGAGCCGGGCGAGAACTGCTTTACCAAGATATCTCTG 4692
QY 3975 GAAGAACTCCAGCATGAGATCCCGCGCTGGAGGATCATCCAGCCGGCGTCCCGGAAAC 4034
DB 4691 TTTGGCCCATATTCAGCTGTTCCATCTGTTCTCTGACCTTGAATCTGAATCTCTATTCTC 4632
QY 4035 GATTCCGAAGCCCAACCTTTTCATAGAAGGGCGGTGGATTCGAATCTCTG----- 4085
DB 4631 AGTTATGTATTTTTCATGCTCTTGCAAAATGGCGTTACTTAAGCTAGTCTGCCAACCTA 4572

QY 4086 -----TGATGGCAGGTTGGCGCTGCTTGGTTCGGTCAAT 4119
Db 4571 CAGGTGGGTCTTTCAATCCCCCTTTTCTGGAGTTGGCGCTGCTTGGTCAAT 4512
QY 4120 TCGAACCCAGAGTCCCGCTCAGAGAACTCGTCAAGAGCGCATAGAGCGCATGCGCT 4179
Db 4511 TCGAACCCAGAGTCCCGCTCAGAGAACTCGTCAAGAGCGCATAGAGCGCATGCGCT 4452
QY 4180 CGGAATCGGAGCGCGCATACCGTAAAGCACAGAGAGCGGTACGCCCATTCGCGGCAA 4239
Db 4451 CGGAATCGGAGCGCGCATACCGTAAAGCACAGAGAGCGGTACGCCCATTCGCGGCAA 4392
QY 4240 GCTCTTCAGCAATATCACGGGTAGCAACGCTATGTCTGTATAGGGTCCGCCACACCA 4299
Db 4391 GCTCTTCAGCAATATCACGGGTAGCAACGCTATGTCTGTATAGGGTCCGCCACACCA 4332
QY 4300 GCCGGCCACAGTCGATGAATCCAGAAAGCGGCCATTTCCACCATGATATTCGGCAAGC 4359
Db 4331 GCCGGCCACAGTCGATGAATCCAGAAAGCGGCCATTTCCACCATGATATTCGGCAAGC 4272
QY 4360 AGGCATCGCCATGGGTCAAGAGATCTCGCGGTGGGCATCGCGGCTTGAAGCTGG 4419
Db 4271 AGGCATCGCCATGGGTCAAGAGATCTCGCGGTGGGCATCGCGGCTTGAAGCTGG 4212
QY 4420 CGAACAGTTCGGCTGGCGGAGCCCTGATGCTCTTCTGTCAGATCATCTGTATGACAA 4479
Db 4211 CGAACAGTTCGGCTGGCGGAGCCCTGATGCTCTTCTGTCAGATCATCTGTATGACAA 4152
QY 4480 GACCGGCTTCATCCGAGTAGTCTCGCTCGATGCGATGTTTGGCTTGGTTCGAATG 4539
Db 4151 GACCGGCTTCATCCGAGTAGTCTCGCTCGATGCGATGTTTGGCTTGGTTCGAATG 4092
QY 4540 GGCAGGTAGCGGATCAAGCGTATGACAGCGCCGCTTGTGATCAGCATGATGATACCT 4599
Db 4091 GGCAGGTAGCGGATCAAGCGTATGACAGCGCCGCTTGTGATCAGCATGATGATACCT 4032
QY 4600 TCTCGCAGGAGCAAGGTGATGACAGAGATCTCGCGGCGCATCTGCCCAATAGCA 4659
Db 4031 TCTCGCAGGAGCAAGGTGATGACAGAGATCTCGCGGCGCATCTGCCCAATAGCA 3972
QY 4660 GCCAGTCCCTTCGCGCTTCAAGTACAGCTGACAGCATGCTGCGAGGAGCGCGCTG 4719
Db 3971 GCCAGTCCCTTCGCGCTTCAAGTACAGCTGACAGCATGCTGCGAGGAGCGCGCTG 3912
QY 4720 TGGCCAGCCAGATAGCGGCTGCTCGTCTGTCAGTTCATTCAGGGCACCGACAGGT 4779
Db 3911 TGGCCAGCCAGATAGCGGCTGCTCGTCTGTCAGTTCATTCAGGGCACCGACAGGT 3852
QY 4780 CGGTCTTTGACAAAAGAACCGGGCGCCCTGCGCTGACAGCGGAAACACCGCGCATCAG 4839
Db 3851 CGGTCTTTGACAAAAGAACCGGGCGCCCTGCGCTGACAGCGGAAACACCGCGCATCAG 3792
QY 4840 AGCAGCCGATGCTGTTGTGCGCCAGTCATAGCGGAATAGCTCTCACCAAGCGGCGG 4899
Db 3791 AGCAGCCGATGCTGTTGTGCGCCAGTCATAGCGGAATAGCTCTCACCAAGCGGCGG 3732
QY 4900 GAGAACCTGCTGCAATCTGTTCAATCATGCGAAGACGATCTCATCTGCTCTCT 4959
Db 3731 GAGAACCTGCTGCAATCTGTTCAATCATGCGAAGACGATCTCATCTGCTCTCT 3672
QY 4960 GATCAGATCTGATCCCTCGCCATCAGATCTCTGCGGCAAGAAAGCCATCCAGTTTA 5019
Db 3671 GATCAGATCTGATCCCTCGCCATCAGATCTCTGCGGCAAGAAAGCCATCCAGTTTA 3612
QY 5020 CTTTGAAGGCTTCCGAACCTTACAGAGGCGGCCAGCTGGCAATTCGGTTCGGTTG 5079
Db 3611 CTTTGAAGGCTTCCGAACCTTACAGAGGCGGCCAGCTGGCAATTCGGTTCGGTTG 3552
QY 5080 CTGTCCATAAAACCGCCAGTCTAGCTATCGCATGTAAGCCCACTGCAAGCTACCTGCT 5139
Db 3551 CTGTCCATAAAACCGCCAGTCTAGCTATCGCATGTAAGCCCACTGCAAGCTACCTGCT 3492
QY 5140 TTCTCTTTGGCTTGGCTTTTCCCTTGTCCAGATAGCCAGTAGCTGACATTCACCGGG 5199

Db 3491 TTCTCTTTGGCTTGGCTTTTCCCTTGTCCAGATAGCCAGTAGCTGACATTCATCCGGG 3432
QY 5200 GTGACGACCGTTCCTGCGGACTGGCTTCTACGTTTCCGCTTCTTTAGCAGCCCTTGC 5259
Db 3431 GTGACGACCGTTCCTGCGGACTGGCTTCTACGTTTCCGCTTCTTTAGCAGCCCTTGC 3372
QY 5260 GCCCTGAGTCTTTCGCGGACGCTG 5283
Db 3371 GCCCTGAGTCTTTCGCGGACGCTG 3348

RESULT 4

US-09-380-190A-30/c
; Sequence 30, Application US/09380190A
; Patent No. 6410220
; GENERAL INFORMATION:
; APPLICANT: NATURE TECHNOLOGY CORPORATION, ET AL.
; TITLE OF INVENTION: SELF-ASSEMBLING GENES, VECTORS AND USES THEREOF

; NUMBER OF SEQUENCES: 74
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MUETING, RAASCH & GEBHARDT, P.A.
; STREET: 119 NORTH FOURTH STREET, SUITE 203
; CITY: MINNEAPOLIS
; STATE: MINNESOTA
; COUNTRY: USA
; ZIP: 55401

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/380,190A
; FILING DATE: 26-Aug-1999
; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US98/03918
; FILING DATE: 28-FEB-98

; ATTORNEY/AGENT INFORMATION:
; NAME: MUETING, ANN M.
; REGISTRATION NUMBER: 33,977
; REFERENCE/DOCKET NUMBER: 228.00010201

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-305-1217
; TELEFAX: 612-305-1228

; INFORMATION FOR SEQ ID NO: 30:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 6561 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 30:

US-09-380-190A-30

Query Match 30.6%; Score 1618.2; DB 3; Length 6561;
Best Local Similarity 86.7%; Pred. No. 0;
Matches 1911; Conservative 0; Mismatches 23; Indels 269; Gaps 1;

QY 3081 GC AAAAGGCCAGCAACCGTAAAGGCGCGGTTGCTGGCGTTTTTCCATAGGCTCCGCCC 3140
Db 2305 GCAGGTGTACTCAGGCGGGCATCTCGCGTTTCTGGCGTTTTTCCATAGGCTCCGCCC 2246
QY 3141 CCCTGACGAGCATCAAAAATCGAGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACT 3200
Db 2245 CCCTGACGAGCATCAAAAATCGAGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACT 2186
QY 3201 ATAAAGATACGAGCGGTTTTCCCGCTTGGAAAGCTCCCTCGTGGCGCTCTCTGTTCCGACCT 3260
Db 2185 ATAAAGATACGAGCGGTTTTCCCGCTTGGAAAGCTCCCTCGTGGCGCTCTCTGTTCCGACCT 2126

TITLE OF INVENTION: Method of Use

NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Suite 4700
STATE: Los Angeles
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472,809B
FILING DATE: June 7, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/209,846
FILING DATE: March 9, 1994
APPLICATION NUMBER: 07/789,919
FILING DATE: No. 592564member 6, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 214/212
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 5707 bases
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-472-809B-8

Query Match 30.3%; Score 1602.2; DB 2; Length 5707;

Best Local Similarity 82.8%; Pred. No. 0;

Matches 2021; Conservative 0; Mismatches 28; Indels 392; Gaps 1;

QY 2706 CTAGAGCTATCATGGTTCATAGCTGTTCTCTGTGTGAATTTGTTATCCGCTCACAATTCC 2765

DB 3514 CTTGGCGTAAATCATGGTTCATAGCTGTTCTGTGTGAATTTGTTATCCGCTCACAATTCC 3573

QY 2766 ACACACATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGTCCTTAATGAGTGAGCTA 2825

DB 3574 ACACACATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGTCCTTAATGAGTGAGCTA 3633

QY 2826 ACTCACATTAATTGCGTTGCGCTCACTGCGCGCTTTCCAGTCGGGAAACCTGTCGTGCCA 2885

DB 3634 ACTCACATTAATTGCGTTGCGCTCACTGCGCGCTTTCCAGTCGGGAAACCTGTCGTGCCA 3693

QY 2886 GCTGCATTAAATGATCGGCCAACCGCGGGGAGAGCGGTTTCGTTATTTGGGCGCTCTTC 2945

DB 3694 GCTGCATTAAATGATCGGCCAACCGCGGGGAGAGCGGTTTCGTTATTTGGGCGCTCTTC 3753

QY 2946 CGCTTCTCGCTCACTGACTCGCTGCGCTCGCTGCGCTCGCTGCGCTCGCTGCGCTCGCTCAGC 3005

DB 3754 CGCTTCTCGCTCACTGACTCGCTGCGCTCGCTGCGCTCGCTGCGCTCGCTGCGCTCGCTCAGC 3813

QY 3006 TCACCTAAAGCGCGTAAATACGGTTATCCACAGAAATCAGGGGATAACCGCAGGAAAGAACAT 3065

DB 3814 TCACCTAAAGCGCGTAAATACGGTTATCCACAGAAATCAGGGGATAACCGCAGGAAAGAACAT 3873

QY 3066 GTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAGGCCGCTGTCGCGCTTTT 3125

DB 3874 GTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAGGCCGCTGTCGCGCTTTT 3933

QY 3126 CCATAGGCTCCGCCCTCCCTGACGAGCATCAAAAAATCGACGCTCAAGTCAGAGGTGGCG 3185
DB 3934 CCATAGGCTCCGCCCTCCCTGACGAGCATCAAAAAATCGACGCTCAAGTCAGAGGTGGCG 3993
QY 3186 AAACCCGACAGGACTATAAAGATACGAGGCGTTTCCCTCGAAGTCCCTCGTGGCGCTC 3245
DB 3994 AAACCCGACAGGACTATAAAGATACGAGGCGTTTCCCTCGAAGTCCCTCGTGGCGCTC 4053
QY 3246 TCCTGTTCCGACCTCGCGCTTACCGGATACCTGTCCGCGCTTCTCCCTTCGGGAAGCGT 3305
DB 4054 TCCTGTTCCGACCTCGCGCTTACCGGATACCTGTCCGCGCTTCTCCCTTCGGGAAGCGT 4113
QY 3306 GCGCGCTTCTCATAGCTCAGCTGTAGGTATCTCAGTTCGGTGTAGGTTCGTCGCTCAA 3365
DB 4114 GCGCGCTTCTCATAGCTCAGCTGTAGGTATCTCAGTTCGGTGTAGGTTCGTCGCTCAA 4173
QY 3366 GCTGGGCTGTGTGACGAAACCCCGTTACGCCGACCGCTGCGCTTATCCGCTAACTA 3425
DB 4174 GCTGGGCTGTGTGACGAAACCCCGTTACGCCGACCGCTGCGCTTATCCGCTAACTA 4233
QY 3426 TCGTCTTTGAGTCCAAACCCCGTTACGCCGACCGCTGCGCTTATCCGCTAACTA 3485
DB 4234 TCGTCTTTGAGTCCAAACCCCGTTACGCCGACCGCTTATCCGCTAACTA 4293
QY 3486 CAGGATTAGCAGAGCGAGGTATGTAGGCGGTCTACAGAGTTCCTTGAAGTGGTGGCTAA 3545
DB 4294 CAGGATTAGCAGAGCGAGGTATGTAGGCGGTCTACAGAGTTCCTTGAAGTGGTGGCTAA 4353
QY 3546 CTACGCTACACTAGAAAGAACAGTATTTGGTATCTCGCTCTGCTGAAGCCAGTTACCTT 3605
DB 4354 CTACGCTACACTAGAAAGAACAGTATTTGGTATCTCGCTCTGCTGAAGCCAGTTACCTT 4413
QY 3606 CGGAAAAGAGTTGGTAGCTCTTGATCCGCAACAAACACCGCTGCTGAGCGGTGGTTT 3665
DB 4414 CGGAAAAGAGTTGGTAGCTCTTGATCCGCAACAAACACCGCTGCTGAGCGGTGGTTT 4473
QY 3666 TTTTGTTCGACGACGACAGATTACGCGCAGAAAAAGAGATCTCAAGAGATCCTTTGAT 3725
DB 4474 TTTTGTTCGACGACGACAGATTACGCGCAGAAAAAGAGATCTCAAGAGATCCTTTGAT 4533
QY 3726 CTTTCTACGGGTCTGACGCTCAGTGGAAACGAAACTCACGTTAAGGGATTTTGGTCAT 3785
DB 4534 CTTTCTACGGGTCTGACGCTCAGTGGAAACGAAACTCACGTTAAGGGATTTTGGTCAT 4551
QY 3786 GAGATTATCGTCACCAAGCGGCACTCGTGCCTCCCACTCTCTGCAAGTTCGGGGCAGT 3845
DB 4552 GAGATTATCGTCACCAAGCGGCACTCGTGCCTCCCACTCTCTGCAAGTTCGGGGCAGT 4551
QY 3846 GATGCGCGATAGCCGCTGCTGGTTTCTGGATGCCGACGGAATTGCACTGCCGCTAGAA 3905
DB 4552 GATGCGCGATAGCCGCTGCTGGTTTCTGGATGCCGACGGAATTGCACTGCCGCTAGAA 4551
QY 3906 CTTCCGCGAGGTGCTCCAGCTCAGGACGAGCTGAACCAACTCGCGAGGGATCGAGCCC 3965
DB 4552 CTTCCGCGAGGTGCTCCAGCTCAGGACGAGCTGAACCAACTCGCGAGGGATCGAGCCC 4551
QY 3966 GGGGTGGCGAAGAACTCCAGCATGAGATCCCGCGCTGGAGGATCATCCAGCCGCGCTC 4025
DB 4552 GGGGTGGCGAAGAACTCCAGCATGAGATCCCGCGCTGGAGGATCATCCAGCCGCGCTC 4551
QY 4026 CCGGAAAACGATTCCGAGCCCAACCTTTTCATAGAAGCGCGGTGGAATCGAAATCTCG 4085
DB 4552 CCGGAAAACGATTCCGAGCCCAACCTTTTCATAGAAGCGCGGTGGAATCGAAATCTCG 4551
QY 4086 TGATGACAGTTGGGCGTCTGTTGGTTCGCTCAATTCGAAACCCAGAGATCCCGCTCAGAAG 4145
DB 4552 TGATGACAGTTGGGCGTCTGTTGGTTCGCTCAATTCGAAACCCAGAGATCCCGCTCAGAAG 4561
QY 4146 AACTCGTCAAGAGCGGATAGAGGCGATCGCTGCGAATCGGAGCGCGGATACCGTAA 4205
DB 4562 AACTCGTCAAGAGCGGATAGAGGCGATCGCTGCGAATCGGAGCGCGGATACCGTAA 4621

2204	Db	GTCTTGAGTCCAAACCCCGGTATAGACACAGACTTATCCCACTGCGCAGCAGCCACTGGTAACA	2144
3488	Qy	GGATTAGCAGAGCGAGGTATGTAGCGGTTGTCTACAGAGTTCTTTGAAGTGGTGGCGCTAACT	3547
2144	Db	GGATTAGCAGAGCGAGGTATGTAGCGGTTGTCTACAGAGTTCTTTGAAGTGGTGGCGCTAACT	2085
3548	Qy	ACGGCTACACTAGAAGAACAGTATTTGGTATCTCGGCTCTGCTGAAGCCAGTTTACCTTCG	3607
2084	Db	ACGGCTACACTAGAAGAACAGTATTTGGTATCTCGGCTCTGCTGAAGCCAGTTTACCTTCG	2025
3608	Qy	GAATAAGATTGGTAGTCTTTGATCCGCGAAACAAACACCGCTGGTAGCGGTGGTTTTT	3667
2024	Db	GAATAAGATTGGTAGTCTTTGATCCGCGAAACAAACACCGCTGGTAGCGGTGGTTTTT	1965
3668	Qy	TTGTTTCAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAAGATCCTTTGATCT	3727
1964	Db	TTGTTTCAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAAGATCCTTTGATCT	1905
3728	Qy	TTTCTACGGGTCTGACGCTCAGTGGAAACGAAACTCAGTTTAAGGGAATTTTGGTCAAGA	3787
1904	Db	TTTCTACGGGTCTGACGCTCAGTGGAAACGAAACTCAGTTTAAGGGAATTTTGGTCAAGA	1845
3788	Qy	GATTATCGTCGACCAAGCGCCATCTGCTCT	3819
1844	Db	GATTATCAAAAAGGATCTTCACTAGATCTCTTTAAATTTAAATGAAGTTTAAATCAA	1785
3820	Qy	-----CCCCACTCTGCAGTTCGGGG	3840
1784	Db	TCATAAGTATATATGAGTAACCTGAGGCTATGCGAGGCGCTGCGCGCCCGACGTTGGCTG	1725
3841	Qy	GCATGGATGCGCGGATAGCGCTGCTGGTTTCTTGGATGCGGACGGAATTTGCACTGCGCG	3900
1724	Db	CGAGCCCTGGCGCTCTCACCGGAACTTGGGGGGTGGGGTGGGAAAGAAAGAAACGCGGG	1665
3901	Qy	-----TAGAACTCCGCGAGGTCGTCCAGCCTCAGCGCAGCAGCTGAACCAAC	3946
1664	Db	CGTATTTGGCCCCAATGGGGTCTCGTGGGGTATCGACAGATGCCAGCCCTGGGACCGAA	1605
3947	Qy	TCGCGAGGGGATCGA-----	3961
1604	Db	CCCCGGTTTATGAAACAAACGACCCACACGCGTGGTTTTATCTGTCTTTTATTTGCCG	1545
3962	Qy	-----GCCCCG	3967
1544	Db	TCATAGCGCGGTTCTTCCGGTATGTCTCTTCCGTGTTTCAGTTAGGCTCCCGCTAG	1485
3968	Qy	GGTGGGCGAAGACTCCAGCATGAGATCCCGCGCTGGAGATCATCCAGCGCGCTCCC	4027
1484	Db	GGTGGGCGAAGAACTCAGCATGAGATCCCGCGCTGGAGATCATCCAGCGCGCTCCC	1425
4028	Qy	GGAACAGATTCCGAAGCCAACTTTCATAGAAGGCGCGGTGGAATCGAAATCTCGTG	4087
1424	Db	GGAACAGATTCCGAAGCCAACTTTCATAGAAGGCGCGGTGGAATCGAAATCTCGTG	1365
4088	Qy	ATGCGAGTTTGGGCGTCCGTTGGTTCGTCATTTTCGAAACCCAGAGTCCCGCTCAGAAGAA	4147
1364	Db	ATGCGAGTTTGGGCGTCCGTTGGTTCGTCATTTTCGAAACCCAGAGTCCCGCTCAGAAGAA	1305
4148	Qy	CTCGTCAAGAAAGGCGATAGAAGGGATGCGCTCGGAATCGGGAGCGCGATACCGTTAAG	4207
1304	Db	CTCGTCAAGAAAGGCGATAGAAGGGATGCGCTCGGAATCGGGAGCGCGATACCGTTAAG	1245
4208	Qy	CACGAGAAAGCGGTACGCCCAATTCCGCGCCAAAGCTCTTTACAGCAATATCACGGGTAGCCAA	4267
1244	Db	CACGAGAAAGCGGTACGCCCAATTCCGCGCCAAAGCTCTTTACAGCAATATCACGGGTAGCCAA	1185
4268	Qy	CGCTATGTCCTGATAGCGGTCGCGCACACCCAGCGCGCCACAGTTCGATGAATCCAGAAA	4327
1184	Db	CGCTATGTCCTGATAGCGGTCGCGCACACCCAGCGCGCCACAGTTCGATGAATCCAGAAA	1125
4328	Qy	GCGGCCATTTTCCAACTATATATTTCCGGAACGAGGCAATCGCCATGCGGTCTACGACAGATC	4387
1124	Db	GCGGCCATTTTCCAACTATATTTCCGGAACGAGGCAATCGCCATGCGGTCTACGACAGATC	1065

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; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 08191/004002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-543-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4665 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-09-169-425C-7

Query Match      29.7%; Score 1571.6; DB 3; Length 4665;
Best Local Similarity 86.3%; Pred. No. 0;
Matches 1850; Conservative 0; Mismatches 114; Indels 180; Gaps 3;

QY 3008 ACTCAAGGCGGTAATACGGTTATCCAGAAATCAGGGGATACCGCAGGAAAGCAATGT 3067
DB 2624 AATGCATGGCGTAATACGGTTATCCACAGAAATCAGGGGATACCGCAGGAAAGCAATGT 2565
QY 3068 GAGCAAAAGCCAGCAAAAGGCCAGGACCGTAAAGGCCGGTTGCTGGCGTTTTC 3127
DB 2564 GAGCAAAAGCCAGCAAAAGGCCAGGACCGTAAAGGCCGGTTGCTGGCGTTTTC 2505
QY 3128 ATAGGCTCGCCGCCCTGACGAGCATCACAAAATCGAAGCTCAAGTCAGAGGTGGCGAA 3187
DB 2504 ATAGGCTCGCCGCCCTGACGAGCATCACAAAATCGAAGCTCAAGTCAGAGGTGGCGAA 2445
QY 3188 ACCCGACAGACTATAAAGATACAGCGGTTTCCCTCGGAAGCTCCCTGTCGCTCTC 3247
DB 2444 ACCCGACAGACTATAAAGATACAGCGGTTTCCCTCGGAAGCTCCCTGTCGCTCTC 2385
QY 3248 CTGTTCCGACCTCGCGCTTACCGGATACCTGTCGCGCTTTCTCCCTTCCGGAAGCGTGG 3307
DB 2384 CTGTTCCGACCTCGCGCTTACCGGATACCTGTCGCGCTTTCTCCCTTCCGGAAGCGTGG 2325
QY 3308 CGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTTCGGGTAGGTGCTGCTCCAAGC 3367
DB 2324 CGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTTCGGGTAGGTGCTGCTCCAAGC 2265
QY 3368 TGGGCTGTGTGCAAGAACCCCGTTACGCCGACCGCTGCGCTTATCCGGTAACTATC 3427
DB 2264 TGGGCTGTGTGCAAGAACCCCGTTACGCCGACCGCTGCGCTTATCCGGTAACTATC 2205
QY 3428 GTCTTGAGTCCAAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACA 3487
DB 2204 GTCTTGAGTCCAAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACA 2145
QY 3488 GGATTAGCAGACGAGTATGTAGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCCTAACT 3547
DB 2144 GGATTAGCAGACGAGTATGTAGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCCTAACT 2085
QY 3548 ACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGGAAGCCAGTTACCTCG 3607
DB 2084 ACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGGAAGCCAGTTACCTCG 2025
QY 3608 GAAAGAGTTGGTGTAGCTCTTGATCCGGCAACAAACACCGCTGGTGGGTGGTTTTT 3667
DB 2024 GAAAGAGTTGGTGTAGCTCTTGATCCGGCAACAAACACCGCTGGTGGGTGGTTTTT 1965
QY 3668 TTCTTTTCAAGCAGCAGATTACCGCAGCAAAAGGATCTCAAGAGATCTCTTTGATCT 3727
DB 1964 TTCTTTTCAAGCAGCAGATTACCGCAGCAAAAGGATCTCAAGAGATCTCTTTGATCT 1905
QY 3728 TTCTCAGGGGTCTGACGCTCAGTGGAAACGAAACTCAAGTTAAGGGATTTTGGTCATGA 3787
DB 1904 TTCTCAGGGGTCTGACGCTCAGTGGAAACGAAACTCAAGTTAAGGGATTTTGGTCATGA 1845
QY 3788 GATTATCGTCGACCAAGGCGGCATCGTGCT----- 3819

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||||| 1844 GATTATCAAAAGGATCTTCACCTAGATCTTTTAAATTAATAAGTATTAATCAA 1785
||||| 3820 -----CCCCACTCTCGATGTTTCGGGG 3840
||||| 1784 TCTAAAGTATATATGAGTAACCTGAGGCTATGCGAGGGCTTCGCCGCCGACGTTGGCTG 1725
||||| 3841 GCATGATGCGCGGATAGCGCTGCTGTTTCTTGATGCCGACGATTTTGACTGCCGG 3900
||||| 1724 CGAGCCCTGGGCTTTACCCGAACTTGGGGGGTGGGGTGGGAAAGGAAGAACCGGG 1665
||||| 3901 -----TAGAACTCCGCGAGGTGCTCAGCCTCAGGAGCAGAGCTGAACCAAC 3946
||||| 1664 CGTATTGGCCCCAATGGGGTCTCGTGGGGTATCGACAGATGCCAGCCCTGGGACCGAA 1605
||||| 3947 TCGCAGGGGATCGA----- 3961
||||| 1604 CCCCGGTTTATGAACAAACGACCAACACCGTGGTTTTATTCTGTCTTTTATTGCGG 1545
||||| 3962 -----GCCCGG 3967
||||| 1544 TCATAGCGGGTTCTTTCGGTATTGTCCTCTCCGTGTTTTCAGTTAGCTTCCCCTAG 1485
||||| 3968 GGTGGCGGAAGAACTCCAGCATGATCCCGCGCTGGAGGATCATCCAGCCGGGTCCC 4027
||||| 1484 GGTGGCGGAAGAACTCCAGCATGATCCCGCGCTGGAGGATCATCCAGCCGGGTCCC 1425
||||| 4028 GGAACACGATTCGGAAGCCAACTTTTCATAGAAGCGCGCGTGAATCGAAATCTCGTG 4087
||||| 1424 GGAACACGATTCGGAAGCCAACTTTTCATAGAAGCGCGCGTGAATCGAAATCTCGTG 1365
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||||| 4148 CTCGTCAAGAGCGCATAGAAGCGATGCGCTGCGAATCGGAGCGCGCATACCGTAAAG 4207
||||| 1304 CTCGTCAAGAGCGCATAGAAGCGATGCGCTGCGAATCGGAGCGCGCATACCGTAAAG 1245
||||| 4208 CACGAGGAGCGGTGAGCCATTCGCCCAAGCTCTTCAGCAATATCAAGGATGCCAA 4267
||||| 1244 CACGAGGAGCGGTGAGCCATTCGCCCAAGCTCTTCAGCAATATCAAGGATGCCAA 1185
||||| 4268 CGCTATGCTGATAGCGGTCCGCCACACCCAGCGCGGCACAGTCGATGTAATCCAGAAA 4327
||||| 1184 CGCTATGCTGATAGCGGTCCGCCACACCCAGCGCGGCACAGTCGATGTAATCCAGAAA 1125
||||| 4328 GCGGCCATTTTCCACCATGATATTGGCAAGCAGGCAATCGCCATGGGTCAAGCAGAGATC 4387
||||| 1124 GCGGCCATTTTCCACCATGATATTGGCAAGCAGGCAATCGCCATGGGTCAAGCAGAGATC 1065
||||| 4388 CTCGCGCTCGGCATGCGCGCTTGAGCTTGCGAAACAGTTTCGGTGGCGGAGCCCCCTG 4447
||||| 1064 CTCGCGCTCGGCATGCTCGCTTCAGCTTGCGAAACAGTTTCGGTGGCGGAGCCCCCTG 1005
||||| 4448 ATGCTCTTCGTCCAGATCATCTGATCGACAGACGGGTTTCATCCCGAGTACGTCTCG 4507
||||| 1004 ATGCTCTTCGTCCAGATCATCTGATCGACAGACGGGTTTCATCCCGAGTACGTCTCG 945
||||| 4508 CTCGATGCGATGTTTCGCTTGGTGTGCAATGGGAGGAGTAGCGGATCAAGCGTATGCAAG 4567
||||| 944 CTCGATGCGATGTTTCGCTTGGTGTGCAATGGGAGGAGTAGCGGATCAAGCGTATGCAAG 885
||||| 4568 CCGCGCATTTGTCATCAGCCATGATGGATATCTTTCTCGGAGGAGCAAGGTGATGATGACAG 4627
||||| 884 CCGCGCATTTGTCATCAGCCATGATGGATATCTTTCTCGGAGGAGCAAGGTGATGATGACAG 825
||||| 4628 GAGATCTCGCCCGCAGCTTCGCCCAATAGCAGCCAGTCCCTTCCGCTTTCAGTACAAAC 4687
||||| 824 GAGATCTCGCCCGCAGCTTCGCCCAATAGCAGCCAGTCCCTTCCGCTTTCAGTACAAAC 765
||||| 4688 GTTCGACGACAGCTGGCGCAAGGAACGCCCGCTCGTGGCCAGCCAGTACGATGAGCGGCTCTC 4747
|||||

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Db 764 GTCAGACACAGCTGGCAGGAACGCCCGTCGTGGCCAGCCACGATAGCCGCGTGCCTC 705
Qy 4748 GTCCTGCAGTTTCATTTCAGGCGACCGGACAGGTCCGTCTTGACAAAAGAACCGGGCGCCC 4807
Db 704 GTCTTGCACTTCATTTCAGGCGACCGGACAGGTCCGTCTTGACAAAAGAACCGGGCGCCC 645
Qy 4808 CTGGCTGACAGCGCGGACACCGCGGCATCAGAGCAGCCGATTCCTGTTGTGCCCCAGTC 4867
Db 644 CTGGCTGACAGCGCGGACACCGCGGCATCAGAGCAGCCGATTCCTGTTGTGCCCCAGTC 585
Qy 4868 ATAGCCGAATAGCTCTCCACCCAAAGCGCGGAGAACCTCGCGTGCATCCATCTTCTTC 4927
Db 584 ATAGCCGAATAGCTCTCCACCCAAAGCGCGGAGAACCTCGCGTGCATCCATCTTCTTC 525
Qy 4928 AATCATGCGAAACGATCCTCATCTCTCTCTTGTATCAGATCTTG 4971
Db 524 AATCATGCGAAACGATCCTCATCTCTCTCTTGTATCAGATCTTG 481

RESULT 8
US-09-759-960-7/c
; Sequence 7, Application US/09759960
; Patent No. 6582704
; GENERAL INFORMATION:
; APPLICANT: Urban, Robert G.
; APPLICANT: Chiciz, Roman M.
; APPLICANT: Collins, Edward J.
; APPLICANT: Hedley, Mary Lynn
; TITLE OF INVENTION: IMMUNOGENIC PEPTIDES FROM THE HPV E7
; TITLE OF INVENTION: PROTEIN
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/759,960
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/169,425
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 08191/004002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-543-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4665 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-09-759-960-7

Query Match 29.7%; Score 1571.6; DB 4; Length 4665;
Best Local Similarity 86.3%; Pred. No. 0;
Matches 1850; Conservative 0; Mismatches 114; Indels 180; Gaps 3;
Qy 3008 ACTCAAGGCGGTAAATCGGTATTCACAGAAATCAGGGGATACCGAGGAAAGAAATGT 3067
Db 2624 AATGCATGGCGGTAAATCGGTATTCACAGAAATCAGGGGATACCGAGGAAAGAAATGT 2565

Qy 3068 GAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAGAGCGCGTGTCTGCGCGTTTTTCC 3127
Db 2564 GAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAGAGCGCGTGTCTGCGCGTTTTTCC 2505
Qy 3128 ATAGGTCTCCGCCCTCTGACGAGATCAAAAATCGACGCTCAAGTCAAGTCAAGTGGCGAA 3187
Db 2504 ATAGGTCTCCGCCCTCTGACGAGATCAAAAATCGACGCTCAAGTCAAGTGGCGAA 2445
Qy 3188 ACCGACAGACTATATAAGATACAGCGGTTTCCCTCGAAGCTCCCTCGTGGCTCTC 3247
Db 2444 ACCGACAGACTATATAAGATACAGCGGTTTCCCTCGAAGCTCCCTCGTGGCTCTC 2385
Qy 3248 CTGTTCCGACCTTCGCGCTTACCGGATACCTGTCGCGCTTTCTCCCTTCGGGAAGCGTGG 3307
Db 2384 CTGTTCCGACCTTCGCGCTTACCGGATACCTGTCGCGCTTTCTCCCTTCGGGAAGCGTGG 2325
Qy 3308 CGCTTTCTCATAGCTCAAGCTGTAGGTATCTCAGTTTCGGTGTAGGTTCGCTTCAAGC 3367
Db 2324 CGCTTTCTCATAGCTCAAGCTGTAGGTATCTCAGTTTCGGTGTAGGTTCGCTTCAAGC 2265
Qy 3368 TGGGCTGTGTGACGAAACCCCGCTTACCGCCGACCGCTGCGCTTATCCGTTAACTATC 3427
Db 2264 TGGGCTGTGTGACGAAACCCCGCTTACCGCCGACCGCTGCGCTTATCCGTTAACTATC 2205
Qy 3428 GTCTTGAGTCCAAACCCCGGTAAAGACACGACTTATCGCCACTGGCAGCAGCACCTGGTAACA 3487
Db 2204 GTCTTGAGTCCAAACCCCGGTAAAGACACGACTTATCGCCACTGGCAGCAGCACCTGGTAACA 2145
Qy 3488 GGATTAGCAGCAGAGGTATGTAGCGGTGCTACAGATTCTTGAAGTGGTGGCTTAACT 3547
Db 2144 GGATTAGCAGCAGAGGTATGTAGCGGTGCTACAGATTCTTGAAGTGGTGGCTTAACT 2085
Qy 3548 ACGGCTACACTAGAAACAGTATTTGGTATCTGCGCTCTGCTGAGCCAGTTTACCTTCG 3607
Db 2084 ACGGCTACACTAGAAACAGTATTTGGTATCTGCGCTCTGCTGAGCCAGTTTACCTTCG 2025
Qy 3608 GAAAAAGAGTTGGTAGCTCTTGATCCGGCAAAACAAACACCGCTGCTAGCGGTGGTTTTT 3667
Db 2024 GAAAAAGAGTTGGTAGCTCTTGATCCGGCAAAACAAACACCGCTGCTAGCGGTGGTTTTT 1965
Qy 3668 TTGTTTGAAGCAGCAGATTACGCGCAGAAAAAGGATCTCAAGAGATCTCTTTGATCT 3727
Db 1964 TTGTTTGAAGCAGCAGATTACGCGCAGAAAAAGGATCTCAAGAGATCTCTTTGATCT 1905
Qy 3728 TTCTACGGGTCTGACGCTCAGTGAACGAAACTCAGTTAAGGATTTTGGTCTATGA 3787
Db 1904 TTCTACGGGTCTGACGCTCAGTGAACGAAACTCAGTTAAGGATTTTGGTCTATGA 1845
Qy 3788 GATTATCGTCGACCAAGCGGCATCGTGCT----- 3819
Db 1844 GATTATCAAAAGGATCTTCACCTAGATCTTTTAAATTAATAATGAAGTTTAAATCAA 1785
Qy 3820 -----CCCCACTCTGCACTTCGGGG 3840
Db 1784 TCTAAAGTATATATAGTAACCTGAGGCTATGCGAGGCTATGCGCGGCTGCGCCCGACGCTGGCTG 1725
Qy 3841 GCATGATCGCGGATAGCGCTGCTGTTTCTGATGCGCAGCGATTTGCACTGCGG 3900
Db 1724 CGAGCCCTGGGCTTTCACCCGAACTTGGGGGGTGGGGGAAAGAAAGAACCGGG 1665
Qy 3901 -----TAGAACTCCGAGGTCTGCTCAGCCTCAGGACGAGCTGAACCAAC 3946
Db 1664 CGTATTGGCCCCAATGGGGTCTCGGTGGGGTATCGACAGAGTGCACCGCTGGACCGGAA 1605
Qy 3947 TCGGAGGGGATCGA----- 3961
Db 1604 CCGCGGTTTATGAACAAACAGCAACACCGTGGTTTTTATTTCTGCTCTTTTATTGCGG 1545
Qy 3962 -----GCCCG 3967
Db 1544 TCATAGCGGGTTCCTTCCGGTATTGCTCTCTTCCGTGTTTCAAGTTAGCTCTCCCTTAG 1485

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QY 3968 GGTGGCGGAGAACTCCAGATGAGATCCCGCGCTGGAGATCATCCAGCCGGCTCC 4027
Db 1484 GGTGGCGGAGAACTCCAGATGAGATCCCGCGCTGGAGATCATCCAGCCGGCTCC 1425
QY 4028 GGAAGGAGTTCGAAAGCCCACTTTCATAGAGCGCGGTGGATCGAAATCTCGTG 4087
Db 1424 GGAAGGAGTTCGAAAGCCCACTTTCATAGAGCGCGGTGGATCGAAATCTCGTG 1365
QY 4088 ATGCGAGTGGCGCTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4147
Db 1364 ATGCGAGTGGCGCTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1305
QY 4148 CTCGTCAGAGCGGATGAGAGCGATGCGCTGCGAATCGGAGCGCGATACCGTAAAG 4207
Db 1304 CTCGTCAGAGCGGATGAGAGCGATGCGCTGCGAATCGGAGCGCGATACCGTAAAG 1245
QY 4208 CAGAGGAGCGGTGAGCCATTCGCGCGCAAGCTCTTCAGCAATATCACGGGTAGCCAA 4267
Db 1244 CAGAGGAGCGGTGAGCCATTCGCGCGCAAGCTCTTCAGCAATATCACGGGTAGCCAA 1185
QY 4268 CGTATGCTGATAGCGGTTCGCGCAACCCAGCGCGGCGCACAGTCGATGAATCCAGAAA 4327
Db 1184 CGTATGCTGATAGCGGTTCGCGCAACCCAGCGCGGCGCACAGTCGATGAATCCAGAAA 1125
QY 4328 GCGGCCATTTCCACCATGATATTCGCGAAGCAGGCGATCGCCATGGTCAAGCAGATC 4387
Db 1124 GCGGCCATTTCCACCATGATATTCGCGAAGCAGGCGATCGCCATGGTCAAGCAGATC 1065
QY 4388 CTCGCGCTGGGCGATGCGCGCTTGGAGCTGGCGAAGCTTCGGCTGGCGGAGCCCTG 4447
Db 1064 CTCGCGCTGGGCGATGCGCGCTTGGAGCTGGCGAAGCTTCGGCTGGCGGAGCCCTG 1005
QY 4448 ATGCTCTTGTGATGATCTGATGATGATGATGATGATGATGATGATGATGATGAT 4507
Db 1004 ATGCTCTTGTGATGATCTGATGATGATGATGATGATGATGATGATGATGATGAT 945
QY 4508 CTCGATGCGATGTTTCGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 4567
Db 944 CTCGATGCGATGTTTCGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 885
QY 4568 CCGCCGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4627
Db 884 CCGCCGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 825
QY 4628 GAGATCTGCGCGGCACTTCGCGCAATAGCAGCAGTCCCTTCCGCTTCAGTGACAAC 4687
Db 824 GAGATCTGCGCGGCACTTCGCGCAATAGCAGCAGTCCCTTCCGCTTCAGTGACAAC 765
QY 4688 GTCGAGCAGCTGCGCAAGGACGCGCTGCGGCGCAGCCAGATAGCGCGCTGCCTC 4747
Db 764 GTCGAGCAGCTGCGCAAGGACGCGCTGCGGCGCAGCCAGATAGCGCGCTGCCTC 705
QY 4748 GTCTTCGAGTTCATTCAGGCGCACCGACAGTTCGCTTTCGACAAAAGAACCGGCGCC 4807
Db 704 GTCTTCGAGTTCATTCAGGCGCACCGACAGTTCGCTTTCGACAAAAGAACCGGCGCC 645
QY 4808 CTCGCTGACAGCCGGAACAACCGCGGCGATCAGAGCAGCGATGCTGTGTGTGCCAGTC 4867
Db 644 CTCGCTGACAGCCGGAACAACCGCGGCGATCAGAGCAGCGATGCTGTGTGTGCCAGTC 585
QY 4868 ATAGCGAATAGCTCTCCACCCAGCGCGGAGAACCTGCTGCAATCCATCTTGTTC 4927
Db 584 ATAGCGAATAGCTCTCCACCCAGCGCGGAGAACCTGCTGCAATCCATCTTGTTC 525
QY 4928 AATCATGCGAAGCAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 4971
Db 524 AATCATGCGAAGCAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 481
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RESULT 9

US-09-380-190A-26

; Sequence 26, Application US/09380190A

; Patent No. 6410220

GENERAL INFORMATION:
APPLICANT: NATURE TECHNOLOGY CORPORATION, ET AL.
TITLE OF INVENTION: SELF-ASSEMBLING GENES, VECTORS AND USES THEREOF

NUMBER OF SEQUENCES: 74
CORRESPONDENCE ADDRESS:
ADDRESSEE: MUEITING, RAASCH & GEBHARDT, P.A.
STREET: 119 NORTH FOURTH STREET, SUITE 203
CITY: MINNEAPOLIS
STATE: MINNESOTA
COUNTRY: USA
ZIP: 55401

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/380,190A
FILING DATE: 28-FEB-98
CLASSIFICATION: <Unknown>
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: PCT/US98/03918
FILING DATE: 28-FEB-98
ATTORNEY/AGENT INFORMATION:
NAME: MUEITING, ANN M.
REGISTRATION NUMBER: 33,977
REFERENCE/DOCKET NUMBER: 228.00010201
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-305-1217
TELEFAX: 612-305-1228

INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 4518 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-09-380-190A-26

Query Match 29.7%; Score 1570; DB 3; Length 4518;

Best Local Similarity 86.2%; Pred. No. 0;

Matches 1849; Conservative 0; Mismatches 115; Indels 180; Gaps 3;

QY	3008	ACTCAAGCGCGTAATACGGTTATCCAGAAATCAGGGGATAAACGAGGAAAGACATGT	3067
Db	1895	AATGCATGGCGGTAATACGGTTATCCACAGAAATCAGGGGATAAACGAGGAAAGACATGT	1954
QY	3068	GAGCAAAAGGCCAGCAAAAGGCCAGAACCGTAAAAAGCCGCTTGGCGGTTTTC	3127
Db	1955	GAGCAAAAGGCCAGCAAAAGGCCAGAACCGTAAAAAGCCGCTTGGCGGTTTTC	2014
QY	3128	ATAGGCTCGCGCCCTCGACGAGCATCAAAAAATCGACGCTCAAGTCAGAGGTGGCGAA	3187
Db	2015	ATAGGCTCGCGCCCTCGACGAGCATCAAAAAATCGACGCTCAAGTCAGAGGTGGCGAA	2074
QY	3188	ACCCGACAGGACTATAAAGATACCAAGCGGTTTCCCGCTGGAAAGCTCCCTCGCGCTCTC	3247
Db	2075	ACCCGACAGGACTATAAAGATACCAAGCGGTTTCCCGCTGGAAAGCTCCCTCGCGCTCTC	2134
QY	3248	CTGTTCGAGCCCTGCGCTTACCGGATACCTGTCGCGCTTTCCTCCCTTCGGGAAGCGTGG	3307
Db	2135	CTGTTCGAGCCCTGCGCTTACCGGATACCTGTCGCGCTTTCCTCCCTTCGGGAAGCGTGG	2194
QY	3308	CGCTTTCATAGCTCACGCTGTAGGTATCTCAGTTTGGGTAGGTGCTTCGCTCCAAGC	3367
Db	2195	CGCTTTCATAGCTCACGCTGTAGGTATCTCAGTTTGGGTAGGTGCTTCGCTCCAAGC	2254
QY	3368	TGGGCTGTGTGACGAAACCCCGCTTACGCCGACCGCTGCGCTTATCCGGTAACTATC	3427
Db	2255	TGGGCTGTGTGACGAAACCCCGCTTACGCCGACCGCTGCGCTTATCCGGTAACTATC	2314

QY 3068 GAGCAAAAGCCAGCAAAAGCCAGGACCGTAAAGCCGCTTCTGGCTGGCTTTTCC 3127
DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
DB 4235 GAGCAAAAGCCAGCAAAAGCCAGGACCGTAAAGCCGCTTCTGGCTGGCTTTTCC 4176
QY 3128 ATAGGCTCCGCCCTCCCTGACGAGCATCAAAAATCGAGCTCAAGTCAAGAGTGGCGAA 3187
DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
DB 4175 ATAGGCTCCGCCCTCCCTGACGAGCATCAAAAATCGAGCTCAAGTCAAGAGTGGCGAA 4116
QY 3188 ACCCGACAGGACTATAAAGATACAGCGGCTTCCCTCGAAGCTCCCTCGTGGCTCTC 3247
DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
DB 4115 ACCCGACAGGACTATAAGATACAGCGGCTTCCCTCGAAGCTCCCTCGTGGCTCTC 4056
QY 3248 CTGCTCCGACCTCCGCTTACCGGATACCTGTCGGCTTCTCCCTTCGGGAGCGTGG 3307
DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
DB 4055 CTGCTCCGACCTCCGCTTACCGGATACCTGTCGGCTTCTCCCTTCGGGAGCGTGG 3996
QY 3308 CGCTTTCTCATAGCTCAGCGCTGAGGTATCTCAGTTTCGGTGTAGGTCTGCTCCCAAGC 3367
DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
DB 3995 CGCTTTCTCATAGCTCAGCGCTGAGGTATCTCAGTTTCGGTGTAGGTCTGCTCCAGC 3936
QY 3368 TGGGCTGTGTGACGAAACCCCGTTACGCCACCGCTGCGCTTATCCGTTAACTATC 3427
DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
DB 3935 TGGGCTGTGTGACGAAACCCCGTTACGCCACCGCTGCGCTTATCCGTTAACTATC 3876
QY 3428 GTCTTGAGTCCAAACCCGTTAAGACACGACTTATCGCCACTGGCAGCAGCACTGGTAA 3487
DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
DB 3875 GTCTTGAGTCCAAACCCGTTAAGACACGACTTATCGCCACTGGCAGCAGCACTGGTAA 3816
QY 3488 GGATTAGCAGAGCGAGTATGTAGCGGTGCTACAGATTCTTGAAGTGTGGCTTAACT 3547
DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
DB 3815 GGATTAGCAGAGCGAGTATGTAGCGGTGCTACAGATTCTTGAAGTGTGGCTTAACT 3756
QY 3548 ACGGCTACACTAGAGAAAGTATTTGGTATCTGCGCTCTGCTGGAAGCAGTTCCTTCG 3607
DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
DB 3755 ACGGCTACACTAGAGAAAGTATTTGGTATCTGCGCTCTGCTGGAAGCAGTTCCTTCG 3696
QY 3608 GAAAAGAGTTGCTAGCTCTTGATCCGGCAAAACAAACCCGCTGCTAGCGGTGGTTTTT 3667
DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
DB 3695 GAAAAGAGTTGCTAGCTCTTGATCCGGCAAAACAAACCCGCTGCTAGCGGTGGTTTTT 3636
QY 3668 TTGTTTGCAAGCAGCAGATTACCGCAGAAAAAAGGATCTCAAGAAGATCTCTTTGATCT 3727
DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
DB 3635 TTGTTTGCAAGCAGCAGATTACCGCAGAAAAAAGGATCTCAAGAAGATCTCTTTGATCT 3576
QY 3728 TTTCTACGGGCTCTGACGCTCAGTGGAAAGAAACTCAAGTTAAGGATTTTGGTCA 3787
DB |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
DB 3575 TTTCTACGGGCTCTGACGCTCAGTGGAAAGAAACTCAAGTTAAGGATTTTGGTCA 3516
QY 3788 GATTATCGTCGACCAAGCGGCCATCGTGCCT----- 3819
DB ||||||| ||||| |||||
DB 3515 GATTATCAAAAAGGATCTTCACCTAGATCTTTTAAATTAATAATGAAGTTTAAATCAA 3456
QY 3820 -----CCCCACTCTCTGCACTTCCGCGCTGCGGG 3840
DB |||||||
DB 3455 TCTAAAGTATATAGTAACCTGAGGCTATGCGAGGCTGCGCGCCGACGTTGCTG 3396
QY 3841 GCATGAGTACGGGATAGCGCTGCTGGTTCTCGATGCGGACGATTTGCACTGCGG 3900
DB |||||||
DB 3395 CGAGCCCTGGGCTTCAACCGAACTTGGGGGGTGGGGTGGGAAAGAAAGAAACGCGG 3336
QY 3901 -----TAGAACTCCGCGAGGTCTGCGAGCCTCAGCAGCAGCTGAACCAAC 3946
DB |||||||
DB 3335 CGTATTGGCCCCAATGGGGTCTCGGTGGGGTATCGACAGAGTCCAGCCCTGGGACCGAA 3276
QY 3947 TCGCGAGGGGATCGA----- 3961
DB |||||||
DB 3275 CCCCGGCTTATGAACAAACGACCAACACCGTGGCTTTTATCTGCTTTTATTGGCG 3216
QY 3962 -----GCCCGG 3967
DB |||||
DB 3215 TCATAGCGCGGTTCTCTCCGTTATGTCTCTCTTCGTTGTTTCAGTTAGCTCCCTCTAG 3156
QY 3968 GGTGGGCGAAGAACTCCAGCATGAGATCCCGCGCTGGAGGATCATCCAGCGCGCTGCC 4027

DB 3155 GGTGGCGAAGAAATCTCAGCATGAGATCCCGCGCTGGAGGATCATCCAGCGCGGCTCCC 3096
QY 4028 GGAACACGATTCGGAAGCCAAACCTTTTCATAGAAGCGCGGTGGAATCGAATCTCGTG 4087
DB |||||||
DB 3095 GGAACACGATTCGGAAGCCAAACCTTTTCATAGAAGCGCGGTGGAATCGAATCTCGTG 3036
QY 4088 ATGGCAGGTTGGGCTGCTTGGTTCGATTTTCGAAACCCAGAGTCCGCTCAGAGAA 4147
DB |||||||
DB 3035 ATGGCAGGTTGGGCTGCTTGGTTCGATTTTCGAAACCCAGAGTCCCGCTCAGAGAA 2976
QY 4148 CTCGTCAGAGCGCATAGAAGCGCATGCGTCCGAAATCGGAGCGCGGATACCGTAAAG 4207
DB |||||||
DB 2975 CTCGTCAGAGCGCATAGAAGCGCATGCGTCCGAAATCGGAGCGCGGATACCGTAAAG 2916
QY 4208 CACGAGGAGCGGTTCAGCCCATTCGCGCAAGCTCTTCAGCAATATATCACGGTTAGCCAA 4267
DB |||||||
DB 2915 CACGAGGAGCGGTTCAGCCCATTCGCGCAAGCTCTTCAGCAATATATCACGGTTAGCCAA 2856
QY 4268 CGCTATGCTCTGATAGCGGTCCGCCACACCCAGCGCGCCACAGTTCGATGAATTCAGAGAA 4327
DB |||||||
DB 2855 CGCTATGCTCTGATAGCGGTCCGCCACACCCAGCGCGCCACAGTTCGATGAATTCAGAGAA 2796
QY 4328 GCGGCCATTTTCCACCATGATATTCGCAAGCAGCATCGCCATGGGTCCAGCAGAGATC 4387
DB |||||||
DB 2795 GCGGCCATTTTCCACCATGATATTCGCAAGCAGCATCGCCATGGGTCCAGCAGAGATC 2736
QY 4388 CTCGCGCTGGGCATCGCGCTTCGAGCTTCGCGAACAGTTCGCGTGGCGCGAGCCCTCG 4447
DB |||||||
DB 2735 CTCGCGCTGGGCATCGCTTCGCTTCGAGCTTCGCGAACAGTTCGCGTGGCGCGAGCCCTCG 2676
QY 4448 ATGCTCTTCGCTCAGATCATCTGATCGACAGACCGGCTTCATCCGAGTACGTTCTCG 4507
DB |||||||
DB 2675 ATGCTCTTCGCTCAGATCATCTGATCGACAGACCGGCTTCATCCGAGTACGTTCTCG 2616
QY 4508 CTCGATTCGATGCTTCGCTTCGTTGGTTCGAAATCGGCGAGGTAGCGGATCAAGCGTATG 4567
DB |||||||
DB 2615 CTCGATTCGATGCTTCGCTTCGTTGGTTCGAAATCGGCGAGGTAGCGGATCAAGCGTATG 2556
QY 4568 CCGCGCATTTGATCAGCCATGATGATATCTTCGCGAGGAGCAAGGTGAGTACAG 4627
DB |||||||
DB 2555 CCGCGCATTTGATCAGCCATGATGATATCTTCGCGAGGAGCAAGGTGAGTACAG 2496
QY 4628 GAGATCTGCCCCCGGCACTTCGCCCAATAGCAGCCAGTCCCTTCGCGTTCAGTACAG 4687
DB |||||||
DB 2495 GAGATCTGCCCCCGGCACTTCGCCCAATAGCAGCCAGTCCCTTCGCGTTCAGTACAG 2436
QY 4688 GTCGAGCAGCTTCGCGAAGGAAACCGCGTTCGTCGCGAGCCAGTACGATGAGTAC 4747
DB |||||||
DB 2435 GTCGAGCAGCTTCGCGAAGGAAACCGCGTTCGTCGCGAGCCAGTACGATGAGTAC 2376
QY 4748 GTCCTGCAAGTTCAATTCAGGGCACCGGACAGGTTCGTTTGAACAAAAGAACCGGGCGCC 4807
DB |||||||
DB 2375 GTCCTGCAAGTTCAATTCAGGGCACCGGACAGGTTCGTTTGAACAAAAGAACCGGGCGCC 2316
QY 4808 CTGCGCTGACCGCGGACACCGCGCATCAGAGCAGCGGATTCGTTGTTGCGGCGAGT 4867
DB |||||||
DB 2315 CTGCGCTGACCGCGGACACCGCGCATCAGAGCAGCGGATTCGTTGTTGCGGCGAGT 2256
QY 4868 ATAGCGCAATAGCTCTCCACCAAGCGCGCGGAGAACCTGGGTGCAATCCATCTTTGTTTC 4927
DB |||||||
DB 2255 ATAGCGCAATAGCTCTCCACCAAGCGCGCGGAGAACCTGGGTGCAATCCATCTTTGTTTC 2196
QY 4928 AATCATGCGAAACGATTCCTCATCTCTGTTCTCTTTGATCAGATCTTG 4971
DB |||||||
DB 2195 AATCATGCGAAACGATTCCTCATCTCTGTTCTCTTTGATCAGATCTTTG 2152

RESULT 11

US-08-751-767A-7/c
; Sequence 7, Application US/08751767A
; Patent No. 5994104
; GENERAL INFORMATION:

APPLICANT: ANDERSON, ROBERT J.
APPLICANT: GRANT, HUGH
APPLICANT: MACDONALD, IAN D.
TITLE OF INVENTION: INTERLUKIN-12 FUSION PROTEIN
NUMBER OF SEQUENCES: 80
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHUYE P. C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/08/751,767A
APPLICATION NUMBER: US/08/751,767A
FILING DATE: 08-NOV-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: SADOFF, B. J.
REGISTRATION NUMBER: 36,663
REFERENCE/DOCKET NUMBER: 117-221
TELECOMMUNICATION INFORMATION:
TELEPHONE: 7038164091
TELEFAX: 7038164100
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 6139 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 3222..4841
US-08-751-767A-7

Query Match 29.78; Score 1570; DB 2; Length 6139;

Best Local Similarity .8628; Pred. No. 0;

Matches 1849; Conservative 0; Mismatches 115; Indels 180; Gaps 3;

QY	3008	ACTCAAAAGCGGTAAATACGGTTATCCACAGATCCAGGGGATAACGAGGAAAGCAACATGT	3067
DB	2624	AATGCATGGCGGTAAATACGGTTATCCACAGATCCAGGGGATAACGAGGAAAGCAACATGT	2565
QY	3068	GAGCAAAAGCGCGAGCAAAAGGCGGAGAACCGTAAAGGCGGTTGCTGGCGTTTTTCC	3127
DB	2564	GAGCAAAAGCGCGAGCAAAAGGCGGAGAACCGTAAAGGCGGTTGCTGGCGTTTTTCC	2505
QY	3128	ATAGGCTCCGCGCGCTGACGAGCATCAAAAATCGACGCTCAAGTCAGAGGTGGCGAA	3187
DB	2504	ATAGGCTCCGCGCGCTGACGAGCATCAAAAATCGACGCTCAAGTCAGAGGTGGCGAA	2445
QY	3188	ACCGCAGGACTATAAAGTACACGAGCTTTCCCGCTGGAAGCTCCCTCGTGGCTCTC	3247
DB	2444	ACCGCAGGACTATAAAGTACACGAGCTTTCCCGCTGGAAGCTCCCTCGTGGCTCTC	2385
QY	3248	CTGTTCGACCTGCGCGCTTACCGGATACCTGCTCCGCTTTTCTCCCTTCGGGAAGCGTGG	3307
DB	2384	CTGTTCGACCTGCGCGCTTACCGGATACCTGCTCCGCTTTTCTCCCTTCGGGAAGCGTGG	2325
QY	3308	CGCTTCTCATAGTCTACGCTGTAGGTATCTCAGTTCCGCTGCTAGGTGCTCCCAAGC	3367
DB	2324	CGCTTCTCATAGTCTACGCTGTAGGTATCTCAGTTCCGCTGCTAGGTGCTCCCAAGC	2265
QY	3368	TGGGCTGTGTCAGAACCCCGCTTCAGCCCGCCGCTGCGCTTATCCGTTAACTATC	3427
DB	2264	TGGGCTGTGTCAGAACCCCGCTTCAGCCCGCCGCTGCGCTTATCCGTTAACTATC	2205
QY	3428	GTCTTGAGTCCAAACCCCGGTAAAGACACGACTTATCGCCACTGGCAGCAGCACTGGTAACA	3487

Db	2204	GTCTTGAGTCCAAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCACTGGTAACA	2145
QY	3488	GGATTAGCAGCAGGAGTATGTAGCGGTGCTACAGAGTCTTTGAAGTGTGGCTTAACCT	3547
DB	2144	GGATTAGCAGCAGGAGTATGTAGCGGTGCTACAGAGTCTTTGAAGTGTGGCTTAACCT	2085
QY	3548	ACGGCTACACTAGAAGAACAGATTTTGGTATCTGCGCTCTGCTGAAGCAGGTACCTTCG	3607
DB	2084	ACGGCTACACTAGAAGAACAGATTTTGGTATCTGCGCTCTGCTGAAGCAGGTACCTTCG	2025
QY	3608	GAAGAAAGAGTTGGTAGCTCTTGATTCGGGCAAAACAAACCCAGCTGTGTAGCGGTGTTTT	3667
DB	2024	GAAGAAAGAGTTGGTAGCTCTTGATTCGGGCAAAACAAACCCAGCTGTGTAGCGGTGTTTT	1965
QY	3668	TTGTTTGAAGCAGCAGATTTACGCGCAGAAAAAAGATCTCAAGAGATCTCTTGTATCT	3727
DB	1964	TTGTTTGAAGCAGCAGATTTACGCGCAGAAAAAAGATCTCAAGAGATCTCTTGTATCT	1905
QY	3728	TTTCTACGGGCTCTGACGCTCAGTGGAAAGAAACTCAGCTTAAGGATTTTGGTCAATGA	3787
DB	1904	TTTCTACGGGCTCTGACGCTCAGTGGAAAGAAACTCAGCTTAAGGATTTTGGTCAATGA	1845
QY	3788	GATTATCGTCGACCAAAAGCGGCATCGTGCTT	3819
DB	1844	GATTATCAAAAAGGATCTTCACTAGATCTTTTAAATTAATAATGAAGTTTAAATCAA	1785
QY	3820	-----CCCCACTCTCGACTTCGGG	3840
DB	1784	TCTAAAGTATATATAGTAACTAGAGCTATGCGAGGCTTGCCTGCGGCTTGGCTG	1725
QY	3841	GCATGATCGCGGATAGCGCTGCTGGTTTCTGATGCGCAGCGATTTGCACTGCGG	3900
DB	1724	CGAGCCTTGGGCTTCCACCGAACTTGGGGGTGGGTGGGAAAGGAAAGAACCGGG	1665
QY	3901	-----TAGAACTCGCGAGGTGCTCCAGCTCAGGCGAGCAGCTGAACCAAC	3946
DB	1664	CGTATTGGCCCAATGGGGTCTCGGTGGGTATCGACAGATGCGCAGCCCGGACCGAA	1605
QY	3947	TCGCGAGGCGGATCGA-----	3961
DB	1604	CCCCCGGTTTATGAACAAACGACCCAAACACCGTGGCTTTTATTCCTCTCTTTTATTCGCG	1545
QY	3962	-----GCCCGG	3967
DB	1544	TCATAGCGCGGTTCTTCCGGTATTTGTTCTCTCTCGTGTTCAGTTAGCTCCCTAG	1485
QY	3968	GGTGGCGAAGAACTCCAGCATGAGATCCCGCGCTGGAGGATCATCCAGCGCGCTCCC	4027
DB	1484	GGTGGCGAAGAACTCCAGCATGAGATCCCGCGCTGGAGGATCATCCAGCGCGCTCCC	1425
QY	4028	GGAAACGATTCGGAAGCCAACTTTTATAGAGCGCGGTGGATCGAATCTCGTG	4087
DB	1424	GGAAACGATTCGGAAGCCAACTTTTATAGAGCGCGGTGGATCGAATCTCGTG	1365
QY	4088	ATGGCAGGTTGGGCTGCTGCTGCTCATTTTGAACCCCGAGTCCCGCTCAGAGAA	4147
DB	1364	ATGGCAGGTTGGGCTGCTGCTGCTCATTTTGAACCCCGAGTCCCGCTCAGAGAA	1305
QY	4148	CTCGTCAAGAGCGGATAGAAGCGATGCGCTGCGAATCGGAGCGCGGATACCGTAAAG	4207
DB	1304	CTCGTCAAGAGCGGATAGAAGCGGATGCGCTGCGAATCGGAGCGCGGATACCGTAAAG	1245
QY	4208	CAGGAGGAGCGGTGAGCCATTCGCGCGCAAGCTCTTCAGCAATATCAGCGGTAGCCAA	4267
DB	1244	CAGGAGGAGCGGTGAGCCATTCGCGCGCAAGCTCTTCAGCAATATCAGCGGTAGCCAA	1185
QY	4268	CGCTATGCTCATAGCGGTGCGCACACCCAGCGCGCACAGTGCATCAATCCAGAAA	4327
DB	1184	CGCTATGCTCATAGCGGTGCGCACACCCAGCGCGCACAGTGCATCAATCCAGAAA	1125
QY	4328	GGCGCATTTTCCACCATGATTTGCGCAAGCAGGCGCATCGCCATGGGTGCGCAGCAGATC	4387

Db	1124	GCGCCATTTCACCATGATATTTCGGCAAGCAGGCGATCGCCATGGGTCAAGCAGATC	1065
Qy	4388	CTGCGCGTGGGCAATCGCGCGCTTGAGCCCTGGCGAAAGTTTCGGCTGGCGGAGCCCTTG	4447
Db	1064	CTGCGCGTGGGCAATCGCGCTTGAGCCCTGGCGAAAGTTTCGGCTGGCGGAGCCCTTG	1005
Qy	4448	ATGCTCTTGGTCAGATCATCTTGATCGACAGACCGGCTTCCATCCGAGTACGTGCTCG	4507
Db	1004	ATGCTCTTGGTCAGATCATCTTGATCGACAGACCGGCTTCCATCCGAGTACGTGCTCG	945
Qy	4508	CTGATGCGCATGTTTCGGCTTGGTGGTTCGAATGGGCAAGTAGCCGATCAAGCGTATGCA	4567
Db	944	CTGATGCGCATGTTTCGGCTTGGTGGTTCGAATGGGCAAGTAGCCGATCAAGCGTATGCA	885
Qy	4568	CCGCGCATTTGCATCAGCCATGATGATATCTTCTCGGAGGACGAAGTGAGATGACAG	4627
Db	884	CCGCGCATTTGCATCAGCCATGATGATATCTTCTCGGAGGACGAAGTGAGATGACAG	825
Qy	4628	GAGATCCTGCCCCGGCACCTTCGCCCAATAGCAGCCAGTCCCTCCCGCTTCAGTGACAA	4687
Db	824	GAGATCCTGCCCCGGCACCTTCGCCCAATAGCAGCCAGTCCCTTCGCCCTTCAGTGACA	765
Qy	4688	GTGAGCACAGCTGCGCAGGAACCGCGTGGGCGAGCAGCATAGCGGCTGCCTC	4747
Db	764	GTGAGCACAGCTGCGCAGGAACCGCGTGGGCGAGCAGCATAGCGGCTGCCTC	705
Qy	4748	GTCTCGAGTTCAATCAGGCGACCGGACAGAGTCTGTTGACAAAAGAACCGGGCGCC	4807
Db	704	GTCTCGAGTTCAATCAGGCGACCGGACAGAGTCTGTTGACAAAAGAACCGGGCGCC	645
Qy	4808	CTGCGCTGACCGCGGCAACCGCGGCATCAGAGCAGCGGATGCTGTGTGTCAGTC	4867
Db	644	CTGCGCTGACCGCGGCAACCGCGGCATCAGAGCAGCGGATGCTGTGTGTCAGTC	585
Qy	4868	ATAGCGAATAGCTCTCCACCAAGCGCGCGAGAACCTGCGTGCAATCCATCTTGTTC	4927
Db	584	ATAGCGAATAGCTCTCCACCAAGCGCGCGAGAACCTGCGTGCAATCCATCTTGTTC	525
Qy	4928	AATCATGCGAAACGATCCTCATCTCTCTCTTGTGATCAGATCTTG	4971
Db	524	AATCATGCGAAACGATCCTCATCTCTCTCTTGTGATCAGATCTTGTG	481

RESULT 12
US-09-796-575-4/c
; Sequence 4, Application US/09796575
; Patent No. 6632671
; GENERAL INFORMATION:
; APPLICANT: Genesegues, Inc.
; TITLE OF INVENTION: NANOCAPSULE ENCAPSULATION SYSTEM AND METHOD
; FILE REFERENCE: G332.12-0001
; CURRENT APPLICATION NUMBER: US/09796, 575
; CURRENT FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: US 60/185, 282
; PRIOR FILING DATE: 2000-02-28
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 4748
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Provided by Dr. Brett Levay-Young of the University of Minnesota
US-09-796-575-4

Query Match	29.7%	Score 1569.8;	DB 4;	Length 4748;
Best Local Similarity	86.3%;	Pred. No. 0;		
Matches 1847;	Conservative 0;	Mismatches 112;	Indels 180;	Gaps 3;
Qy	3013	AAGCGGTAAATACGGTTTATCCAGAGATCAGGGGATAACGAGAAAGAACATGTGACCA	3072	
Db	4744	ATGCGGTAAATACGGTTTATCCAGAGATCAGGGGATAACGAGAAAGAACATGTGTGACCA	4685	

Qy	3073	AAAGCCAGCAAAAGCCAGGAAACCGTAAAGAGCCGCGTTCGTGCGCGTTTTTCCATAGG	3132
Db	4684	AAAGCCAGCAAAAGCCAGGAAACCGTAAAGAGCCGCGTTCGTGCGCGTTTTTCCATAGG	4625
Qy	3133	CTCCGCCCCCTTGACAGAGCATCACAAAATCGACGCTCAAGTCAGAGTGGCGAAACCGG	3192
Db	4624	CTCCGCCCCCTTGACAGAGCATCACAAAATCGACGCTCAAGTCAGAGTGGCGAAACCGG	4565
Qy	3193	ACAGACTATATAAGATACACAGCGCTTCCCTCGAAGCTCCCTCGTGGCTCTCTGTT	3252
Db	4564	ACAGACTATATAAGATACACAGCGCTTCCCTCGAAGCTCCCTCGTGGCTCTCTGTT	4505
Qy	3253	CCGACCTTCCGCTTACCGGATACCTGTCGCGCTTTCCTTCCGGAAGCGTGGCGTT	3312
Db	4504	CCGACCTTCCGCGCTTACCGGATACCTGTCGCGCTTTCCTTCCGGAAGCGTGGCGTT	4445
Qy	3313	TCTCATAGCTCACGCTGTAGGTATCTCAGTTTCGGTGTAGGTTCGTTCGCTCCAAGCTGGGC	3372
Db	4444	TCTCATAGCTCACGCTGTAGGTATCTCAGTTTCGGTGTAGGTTCGTTCGCTCCAAGCTGGGC	4385
Qy	3373	TGTGTGCAAGAACCCCGCTTACGCGCAGCCGCTCGGCTTATCCGGTAAACTATCGTCT	3432
Db	4384	TGTGTGCAAGAACCCCGCTTACGCGCAGCCGCTCGGCTTATCCGGTAAACTATCGTCT	4325
Qy	3433	GAGTCCAAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAAACAGGATT	3492
Db	4324	GAGTCCAAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAAACAGGATT	4265
Qy	3493	AGCAGAGCAGGATATGTAGGCGGTCTACAGAGTTCTTTGAAGTGGTGGCTTAACTACGCG	3552
Db	4264	AGCAGAGCAGGATATGTAGGCGGTCTACAGAGTTCTTTGAAGTGGTGGCTTAACTACGCG	4205
Qy	3553	TACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAATA	3612
Db	4204	TACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAATA	4145
Qy	3613	AGAGTTGGTAGCTCTTGATCCGGCAAAACAAACACCGCTGGTAGCGGTGGTTTTTGT	3672
Db	4144	AGAGTTGGTAGCTCTTGATCCGGCAAAACAAACACCGCTGGTAGCGGTGGTTTTTGT	4085
Qy	3673	TGCAAGCAGCAGATTTACGCGCAGAAAAAAGGATCTCAAGAGATCTTTTGATCTTTCT	3732
Db	4084	TGCAAGCAGCAGATTTACGCGCAGAAAAAAGGATCTCAAGAGATCTTTTGATCTTTCT	4025
Qy	3733	ACGGGCTGACGCTCAGTGGAAAGAAACCTCAGCTTAAGGATTTGGTCAATGAGATTA	3792
Db	4024	ACGGGCTGACGCTCAGTGGAAAGAAACCTCAGCTTAAGGATTTGGTCAATGAGATTA	3965
Qy	3793	TCGTGCAACCAAGCGGCATCGTGCT-----	3819
Db	3964	TCAAAAGGATCTTCACTAGATCTTTTAAATTAAGATTTTAAATCAATCTTAA	3905
Qy	3820	-----CCCACTCTGACAGTTTCGGGGGCGATG	3845
Db	3904	AGTATATAGCTAACCTGAGGCTATGGCAGGCGCTGCGGCCCGACGCTTGGCTGCGAGC	3845
Qy	3846	GATGCGCGGATAGCCGCTGCTGTTTCTGATAGCCGAGGATTTGCACTGCGCG-----	3900
Db	3844	CCTGGGCTTTCACCCGAACTTGGGGGTGGGGTGGGAAAGAAAGAAACGCGGGCGTAT	3785
Qy	3901	-----TAGAACTCCGCGAGGTCGTCACGCTCAGCAGCAGCTGAACCACTCGG	3951
Db	3784	TGGCCCCAATGGGCTCGTGGGTATCGACAGAGTGCACCCCTGGGACCGAACCCCG	3725
Qy	3952	AGGGGATCGA-----	3961
Db	3724	CGTTTATGAACAAACGACCCACACCGTGGTTTTTATTCTGTCTTTTATTGCGGTCA	3665
Qy	3962	-----GCCCGGGTGG	3972
Db	3664	GCGCGGTTCTTCCGGTATTTGCTCTTCCGTTTTCAGTTTTCAGCTTCCCTCCCTAGGGTGG	3605
Qy	3973	GCGAAGAACTCCAGCATGAGATCCCGCGCTGAGGATCATCCAGCAGCGCGTCCCGGAAA	4032

3604	Db	CGGAGNACTTCAGCATAGATCCC CGCTGGAGGATCATCAGCGCGGTCCCGAAA	3545
4033	Qy	ACGATTCGGAAGCCCAACCTTTTCATAGAAGCGCGCGTGAATCGAAATCTCGTAGTGGC	4092
3544	Db	ACGATTCGGAAGCCCAACCTTTTCATAGAAGCGCGCGTGAATCGAAATCTCGTAGTGGC	3485
4093	Qy	AGGTTGGGCGTCCGTTGGTCGGTCAATTTCCAAACCCAGAGTCCCGCTCAGAAGAACCTCGT	4152
3484	Db	AGGTTGGGCGTCCGTTGGTCGGTCAATTTCCAAACCCAGAGTCCCGCTCAGAAGAACCTCGT	3425
4153	Qy	CAGAAGGCGATAGAAGCGATCGCTGCGAATCGGAGCGGCGATACCGTAAAGCACGA	4212
3424	Db	CAGAAGGCGATAGAAGCGATCGCTGCGAATCGGAGCGGCGATACCGTAAAGCACGA	3365
4213	Qy	GGNAGCGGTGAGCCCAATTCGCGCGCAAGCTCTTCAGCAATATCACGGGTAGCCAAACGCTA	4272
3364	Db	GGNAGCGGTGAGCCCAATTCGCGCGCAAGCTCTTCAGCAATATCACGGGTAGCCAAACGCTA	3305
4273	Qy	TGTCCTGATAGCGGTCCGCCACACCCAGCGGCCACAGTCGATGAATCCAGAAAAAGCGGC	4332
3304	Db	TGTCCTGATAGCGGTCCGCCACACCCAGCGGCCACAGTCGATGAATCCAGAAAAAGCGGC	3245
4333	Qy	CAATTTTCCACCATGATATTTCGGCAAGCAGTCGCAATCGGATCGGATCCTCGC	4392
3244	Db	CAATTTTCCACCATGATATTTCGGCAAGCAGTCGCAATCGGATCGGATCCTCGC	3185
4393	Qy	CGTCGGGATGCGCGCTTCAGCGCTCGGCAACAGTTTCGGCTGGCGGAGCCCTGATGCT	4452
3184	Db	CGTCGGGATGCTCGCGCTTCAGCGCTCGGCAACAGTTTCGGCTGGCGGAGCCCTGATGCT	3125
4453	Qy	CTTTCGTCAGATCATCTCGATCGACAAAGACCGGCTTCATCCGAGTACGTGCTCGTTCGA	4512
3124	Db	CTTTCGTCAGATCATCTCGATCGACAAAGACCGGCTTCATCCGAGTACGTGCTCGTTCGA	3065
4513	Qy	TGGGATGTTTTCGTTGGTGGTTCGAATGGGAGAGTACGCGATCAAGGTTATGAGCGCGCC	4572
3064	Db	TGCGATGTTTTCGTTGGTGGTTCGAATGGGAGAGTACGCGATCAAGGTTATGAGCGCGCC	3005
4573	Qy	GCATTCGATCAGCCATGATGGATACCTTCTCGCAGCAGCAAGGTGAGATGACAGAGAT	4632
3004	Db	GCATTCGATCAGCCATGATGGATACCTTCTCGCAGCAGCAAGGTGAGATGACAGAGAT	2945
4633	Qy	CTTGCCCCGGCATTCGCCCCAATAGCAGCCAGTCCCTTCCCGTTTCAGTGACAAACGTCGA	4692
2944	Db	CTTGCCCCGGCATTCGCCCCAATAGCAGCCAGTCCCTTCCCGTTTCAGTGACAAACGTCGA	2885
4693	Qy	GCACAGCTCGCAAGGAACGCCCGTCTGTCGACAGCCACGATAGCCGCTGCTCGCTCCT	4752
2884	Db	GCACAGCTCGCAAGGAACGCCCGTCTGTCGACAGCCACGATAGCCGCTGCTCGCTCCT	2825
4753	Qy	GCAGTTTCATTTCAGGGCACCGGACAGGTTCGGTCTTTGACAAAAGAACCGGGCGCCCTCGC	4812
2824	Db	GCAGTTTCATTTCAGGGCACCGGACAGGTTCGGTCTTTGACAAAAGAACCGGGCGCCCTCGC	2765
4813	Qy	CTGACAGCCGGAACACGGCGGCAATCAGACAGCCGATTTGTTCTGTTGCCCCAGTCATAGC	4872
2764	Db	CTGACAGCCGGAACACGGCGGCAATCAGACAGCCGATTTGTTCTGTTGCCCCAGTCATAGC	2705
4873	Qy	CGAATAGCTCTCTCCACCCAAAGCGGCCGAGAACCTCGTCGAATCCATCTTGTTCATCA	4932
2704	Db	CGAATAGCTCTCTCCACCCAAAGCGGCCGAGAACCTCGTCGAATCCATCTTGTTCATCA	2645
4933	Qy	TGCGAAACGATCTCATCTCTGCTCTTTGATCAGATCTTG	4971
2644	Db	TGCGAAACGATCTCATCTCTGCTCTTTGATCAGATCTTG	2606

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/ APPLICANT: Genesegues, Inc.
/ TITLE OF INVENTION: NANOCAPSULE ENCAPSULATION SYSTEM AND METHOD
/ FILE REFERENCE: G3332.12-0001
/ CURRENT APPLICATION NUMBER: US/09/796,575
/ CURRENT FILING DATE: 2001-02-28
/ PRIOR APPLICATION NUMBER: US 60/185,282
/ PRIOR FILING DATE: 2000-02-28
/ NUMBER OF SEQ ID NOS: 5
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 5
/ LENGTH: 4992
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Supplied by BD Biosciences Clontech of Pal
US-09-796-575-5

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	Query Match	29.7%	Score 1569.8	DB 4	Length 4992	
	Best Local Similarity	86.3%	Pred. No. 0			
	Matches 1847	Conservative 0	Mismatches 112	Indels 180	Gaps 3	
QY	3013	AAGGCGGTAAATACGGTTATCCACAGAAATCAGGGGATAACGCAGGAAAGACATGTGAGCA	3072			
Db	4988	ATGGCGGTAAATACGGTTATCCACAGAAATCAGGGGATAACGCAGGAAAGACATGTGAGCA	4929			
QY	3073	AAAGGCCAGCAAAAGGCCAGGAACCGCTAAAGGCCCGCGTTGCTGGCGTTTTTCCATAGG	3132			
Db	4928	AAAGGCCAGCAAAAGGCCAGGAACCGCTAAAGGCCCGCGTTGCTGGCGTTTTTCCATAGG	4869			

RESULT 13
US-09-796-575-5/c
; Sequence 5, Applicat
; Patent No. 6632671
; GENERAL INFORMATION:


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QY 3793 TCCTGACCAAGCGCCATCGTGCT----- 3819
Db 4208 TCAAAAGGATCTTACCTAGATCTCTTTAAATTAATAATGAAGTTTAAATCAATCTAA 4149
QY 3820 -----CCCCACTCTCTGAGTTCGGGGGCGATG 3845
Db 4148 AGTATATAGTAACCTGAGGCTATGGCAGGCGCTGCCGCCCGAGCTTGGCTGGAGC 4089
QY 3846 GATCGCGGATAGCGCTGCTGTTCTTGATGCCGACGATTTGCACTGCGG----- 3900
Db 4088 CTTGGGCTTACCCGAACTTGGGGGGTGGGGGAAAGAAAGAAACGCGGGCGTAT 4029
QY 3901 -----TAGAACTCCGCGAGTCTGCAGCCTCAGCAGCAGCTGAACCAACTCGCG 3951
Db 4028 TGGCCCCATGGGGTCTGGTGGGGTATCGAAGAGTGCAGCCCTGGGACCGAACCCCG 3969
QY 3952 AGGGATCGA----- 3961
Db 3968 CGTTTATGAACAAACGACCAACACCGTGGTTTTATTCTGTCTTTATTGCGGTCA 3909
QY 3962 -----GCCGGGGTGG 3972
Db 3908 GCGCGGGTCTTCCGGTATTTGTCCTTCCGTGTTTCAGTTAGCTCCCTCCTAGGGTGG 3849
QY 3973 GCGAAGAACTCCAGCATGATCCCGCGCTGGAGGATCATCCAGCGCGGCTCCCGAAA 4032
Db 3848 GCGAAGAACTCCAGCATGATCCCGCGCTGGAGGATCATCCAGCGCGGCTCCCGAAA 3789
QY 4033 ACGATTCCGAAGCCCAACCTTTTCATAGAAGCGCGGTGGAATCGAAATCTCGTATGGC 4092
Db 3788 ACGATTCCGAAGCCCAACCTTTTCATAGAAGCGCGGTGGAATCGAAATCTCGTATGGC 3729
QY 4093 AGTTGGGCGTCTGCTGCTGCTATTTGAAACCCAGAGTCCCGCTCAGAGAACTCGT 4152
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QY 4153 CRAAGAAGGATAGAAGGCGATCGCTGCGAATCGGAGCGGGGATACCGTAAAGCACGA 4212
Db 3668 CAAGAAGGCGATAGAAGGCGATCGCTGCGAATCGGAGCGGGGATACCGTAAAGCACGA 3609
QY 4213 GGAAGCGGTGAGCCCAATTCGCCGCCAAGCTCTTCAGCAATATCACGGGTAGCCAAACGCTA 4272
Db 3608 GGAAGCGGTGAGCCCAATTCGCCGCCAAGCTCTTCAGCAATATCACGGGTAGCCAAACGCTA 3549
QY 4273 TGTCTGTATAGCGGTTCGCCACACCCAGCGGCCACAGTCGATGAATCCAGAAACCGGC 4332
Db 3548 TGTCTGTATAGCGGTTCGCCACACCCAGCGGCCACAGTCGATGAATCCAGAAACCGGC 3489
QY 4333 CATTTTCCACCATGATATTCGGCAAGCAGCATCGCCATGGGTACAGCAGATCCTCGC 4392
Db 3488 CATTTTCCACCATGATATTCGGCAAGCAGCATCGCCATGGGTACAGCAGATCCTCGC 3429
QY 4393 CGTGGGCGATCGCGCTTGAGCTTGCGCAACAGTTTCGGCTGGCGGAGCCCTGATGCT 4452
Db 3428 CGTGGGCGATCGCGCTTGAGCTTGCGCAACAGTTTCGGCTGGCGGAGCCCTGATGCT 3369
QY 4453 CTTGCTCCAGATCATCTGTATGACAAAGACCGGTTCCATCCAGTACGTGCTGCTCGA 4512
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Db 3308 TCGATGTTTTCGCTTGGTTCGAATGGGCGAGGTAGCCGATCAAGCGTATGACGCGGC 3249
QY 4573 GCATTGCATCAGCCATGATGATACCTTTCTCGGCAGGAGCAAGGTGAGATGACAGGAGAT 4632
Db 3248 GCATTGCATCAGCCATGATGATACCTTTCTCGGCAGGAGCAAGGTGAGATGACAGGAGAT 3189
QY 4633 CTTGCCCGCGCATCTTCCGCCAAATAGCAGCGAGTCCCTTCCCGCTTCAGTGACAAAGTGA 4692
Db 3188 CTTGCCCGCGCATCTTCCGCCAAATAGCAGCGAGTCCCTTCCCGCTTCAGTGACAAAGTGA 3129
QY 4693 GCACAGCTGGCAAGGAACGCCCGTCTGTGGCCAGCCAGATAGCCGCGCTCGTCTCT 4752
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Db 3128 GCACAGCTGGCAAGAACGCCCGTGTGGCCAGCCACGATAGCCGCGCTGCTCGTCT 3069
QY 4753 GCAGTTTCATTCAGGCGACCCGACAGGTGCTGTTCGACAAAAGAACCCGGGCGCCCTGGC 4812
Db 3068 GCAGTTTCATTCAGGCGACCCGACAGGTGCTGTTCGACAAAAGAACCCGGGCGCCCTGGC 3009
QY 4813 CTGACAGCCGGAACACCGCGGCATCAGACGACCGCATGCTGTGTGTGTCGCCAGTCATAGC 4872
Db 3008 CTGACAGCCGGAACACCGCGGCATCAGACGACCGCATGCTGTGTGTGTCGCCAGTCATAGC 2949
QY 4873 CGAATAGCTCTTCCACCAAGCGCGCGAGAACCTGCGTGCATCATCTTGTTCATCA 4932
Db 2948 CGAATAGCTCTTCCACCAAGCGCGCGAGAACCTGCGTGCATCATCTTGTTCATCA 2889
QY 4933 TCGCAACGATCCTCATCTGCTCTTGTGATCAGATCTTG 4971
Db 2888 TCGCAACGATCCTCATCTGCTCTTGTGATCAGATCTTG 2850

RESULT 14
US-09-393-483A-1/c
; Sequence 1, Application US/09393483A
; Patent No. 6689936
; GENERAL INFORMATION:
; APPLICANT: Burgess, Robert
; APPLICANT: Amano, Satoshi
; APPLICANT: Kishimoto, Jiro
; APPLICANT: Nishiyama, Toshio
; APPLICANT: Ehama, Ritsuko
; TITLE OF INVENTION: METHODS FOR EVALUATING A COMPOUND FOR
; FILE REFERENCE: 10287-054001
; CURRENT APPLICATION NUMBER: US/09393,483A
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 09/070,436
; PRIOR FILING DATE: 1998-04-30
; PRIOR APPLICATION NUMBER: 60/069,945
; PRIOR FILING DATE: 1997-12-17
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 5069
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-393-483A-1

Query Match 29.7%; Score 1569.8; DB 4; Length 5069;
Best Local Similarity 86.3%; Pred. No. 0;
Matches 1847; Conservative 0; Mismatches 112; Indels 180; Gaps 3;

QY 3013 AAGCGGTTAATACGGTTATCCAGAAATCAGGGGATACGAGGAAAGAACATGTGAGCA 3072
Db 5065 ATGGCGGTTAATACGGTTATCCACAGAAATCAGGGGATACGAGGAAAGAACATGTGAGCA 5006
QY 3073 AAAGCCCAAGAAAGCCAGGAACCGTAAAGAGCGCGTCTGCTGCGTTTTTCCATAGC 3132
Db 5005 AAAGCCCAAGAAAGCCAGGAACCGTAAAGAGCGCGTCTGCTGCGTTTTTCCATAGC 4946
QY 3133 CTCGCGCCCTTCAGAGCATCAAAAATCGACGCTCAAGTCAGAGGTGGGAAACCCG 3192
Db 4945 CTCGCGCCCTTCAGAGCATCAAAAATCGACGCTCAAGTCAGAGGTGGGAAACCCG 4886
QY 3193 ACAGGACTATAAGATACAGGGGTTTCCCTCGAAGCTCCCTGCTGCTCTCTGTT 3252
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RESULT 15

US-09-393-483A-2

; Sequence 2, Application, US/09393483A

; Patent No. 6689936

; GENERAL INFORMATION:

; APPLICANT: Burgeson, Robert

; APPLICANT: Amano, Satoshi

; APPLICANT: Kishimoto, Jiro

; APPLICANT: Nishiyama, Toshio

; APPLICANT: Ehama, Ritsuko

; TITLE OF INVENTION: METHODS FOR EVALUATING A COMPOUND FOR ITS EFFECT ON SKIN

; FILE REFERENCE: 10287-054001

; CURRENT APPLICATION NUMBER: US/09/393,483A

; CURRENT FILING DATE: 1999-09-10

; PRIOR APPLICATION NUMBER: 09/070,436

; PRIOR FILING DATE: 1998-04-30

; PRIOR APPLICATION NUMBER: 60/069,945

; NUMBER OF SEQ ID NOS: 7

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 2

; LENGTH: 5069

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GenCore version 5.1.6
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(without alignments)

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	1697.8	32.1	4187	21	US-10-811-028A-6
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9	1697.8	32.1	5753	21	US-10-811-028A-3	Sequence 3, Appl
10	1697.8	32.1	5760	21	US-10-811-028A-4	Sequence 4, Appl
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33	1603.8	30.4	3534	18	US-10-315-907A-15	Sequence 15, Appl
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39	1603.8	30.4	3534	19	US-10-281-067B-15	Sequence 15, Appl
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43	1603.8	30.4	3534	19	US-10-699-597A-10	Sequence 10, Appl
44	1603.8	30.4	3534	19	US-10-166-356-7	Sequence 7, Appl
45	1603.8	30.4	3534	19	US-10-166-356-8	Sequence 8, Appl

ALIGNMENTS

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; Sequence 36, Application US/09921143
; Publication No. US20030215921A1
; GENERAL INFORMATION:
; APPLICANT: Coleman, Timothy
; TITLE OF INVENTION: Vascular Endothelial Growth Factor-2
; FILE REFERENCE: PFI12P6
; CURRENT APPLICATION NUMBER: US/09/921,143
; CURRENT FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 60/223,276
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 36
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; TYPE: DNA
; ORGANISM: homo sapiens
US-09-921-143-36

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DB 3061 AACATGTAGCAAAAGGCGAGCAAAAGGCGAGCAAAAGGCGGGTGGTGGCG 3120
QY 3121 TTTTTCATAGGCTCCGCCCCCTGACGAGCATCAAAAATCAGCGCTCAAGTCAGAGG 3180
DB 3121 TTTTTCATAGGCTCCGCCCCCTGACGAGCATCAAAAATCAGCGCTCAAGTCAGAGG 3180
QY 3181 TGGCGAAACCCGACAGGACTATAAGATACAGGCGGTTTCCCGCTGGAGCTCCCTCGTG 3240
DB 3181 TGGCGAAACCCGACAGGACTATAAGATACAGGCGGTTTCCCGCTGGAGCTCCCTCGTG 3240
QY 3241 CGCTCTCTGTTCCGACCTCGCGCTTACCGGATACCTGTCCGCTTTCTCCCTCGGGA 3300
DB 3241 CGCTCTCTGTTCCGACCTCGCGCTTACCGGATACCTGTCCGCTTTCTCCCTCGGGA 3300
QY 3301 AGCGTGGCGCTTCTCATAGCTCAGCGCTGAGGTATCTCAGTTCGGGTGAGTTCGTCG 3360
DB 3301 AGCGTGGCGCTTCTCATAGCTCAGCGCTGAGGTATCTCAGTTCGGGTGAGTTCGTCG 3360
QY 3361 TCCAAAGCTGGGCTGTGTGACGAAACCCCGGTTTCCAGCCCGCTTATCCGGT 3420

DB 3361 TCCAAAGCTGGGCTGTGTGACGAAACCCCGTTTCCAGCCCGCTTATCCGGT 3420
QY 3421 AACCTATCGCTTCAGTCCACCCGGTAAAGACAGACTTATCGCACTTGGCAGCAGCCACT 3480
DB 3421 AACCTATCGCTTCAGTCCACCCGGTAAAGACAGACTTATCGCACTTGGCAGCAGCCACT 3480
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DB 3481 GGTAAACAGGATTAAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTTGAAGTGGTG 3540
QY 3541 CCTAACTACGGCTACCTAGAGAAACAGTATTTGGTATCTGCGCTCTGCTGAAAGCCAGTT 3600
DB 3541 CCTAACTACGGCTACCTAGAGAAACAGTATTTGGTATCTGCGCTCTGCTGAAAGCCAGTT 3600
QY 3601 ACCTTCGGAAAAAGAGTGTGTAGCTCTTGATCCGGCAAAACAAACCCCGCTGGTAGCGGT 3660
DB 3601 ACCTTCGGAAAAAGAGTGTGTAGCTCTTGATCCGGCAAAACAAACCCCGCTGGTAGCGGT 3660
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DB 3661 GGTTTTTTTTGTGCAAGCAGCAGATTAAGCGCAGAAAAAAGGATCTCAAGAAAGATCCT 3720
QY 3721 TTGATCTTTTCTACGGGGTCTGACGCTCAGTGGAACGAAAACTCAGCTTAAGGGAATTTTG 3780
DB 3721 TTGATCTTTTCTACGGGGTCTGACGCTCAGTGGAACGAAAACTCAGCTTAAGGGAATTTTG 3780
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DB 3781 GTCATCAGATTAATCGTCGACCAAAAGCGGCATCGTGCCTCCCACTCTCGCAGTTCGGGG 3840
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DB 3901 TAGAACTCCGCGAGTGTCTCAGCTCAGCGAGCAGCTGAAACCACTCGCGAGGGGATCG 3960
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DB 3961 AGCCCGGGTGGCGAGAACTCAGCATGAGATCCCGGCTGGAGGATCATCCAGCGG 4020
QY 4021 GGGTCCCGGAAACGATTCGAAAGCCCAACCTTTATAGAGGCGCGGTGGAATCGAAA 4080
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DB 4081 TCTCTGATGGCAGGTTGGGCGTGGTGGTCAATTTGAAACCCCAAGTTCGCGCTC 4140
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QY 4261 TAGCCAAACGCTATGTCCTGATAGCGGTCCGCCACACCCAGCGCGCCACAGTCGATGAAATC 4320
DB 4261 TAGCCAAACGCTATGTCCTGATAGCGGTCCGCCACACCCAGCGCGCCACAGTCGATGAAATC 4320
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DB 4321 CAGAAAGCGGCGCATTTTCCATGATATTCGGAGCAGGATCGCCATGGGTACCGA 4380
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DB 4381 CGAGATCTCTCGCGTGGGCGATCGCGCGCTTGAGCCTGCGCAACAGTTCGGTGGCGCGCA 4440
QY 4441 GCGCCTGATGCTCTTCTGTCAGATCATCTCTGATTCGAAAGCGGCTTCCATCCGAGTAC 4500

Db	9108	CTTGGCGTAAATCATGTCATAGCTGTTCTGTGTGAATTTGTTATCCGCTCACATTC	10188	GAGATTATCAAAAGGATCTTTCACCTAGATCCTT	10221
QY	2766	ACACAACATACGAGCCGGAAGCATAAAGTGTAAAGCCTCGGGTGCTTAATGATGAGCTA	3846	GATGCGCGATAGCCGCTGCTGTTTCTGTGATGCCGACGGATTTGCACTGCCGCTAGAA	3905
Db	9168	ACACAACATACGAGCCGGAAGCATAAAGTGTAAAGCCTCGGGTGCTTAATGATGAGCTA	10222		10221
QY	2826	ACTCACATTAATTTGCGTTGGCTCACTGCGCGCTTTCCAGTCGGGAAACCTGTGTGCCA	3906	CTCCGCGAGGTGCTCCAGCCTCAGSCAGCAGCTGAACCACTCGCGAGGGATCGAGCC	3965
Db	9228	ACTCACATTAATTTGCGTTGGCTCACTGCGCGCTTTCCAGTCGGGAAACCTGTGTGCCA	10222		10223
QY	2886	GCTGCATTAATGAATCGGCCAAACGCGCGGAGAGCGGTTTGCATTTGGCGCTCTTC	3966	GGGTGGCGCAAGAACTCCAGCATGAGATCCCGCGCTGGAGGATCATCCAGCCGCGTC	4025
Db	9288	GCTGCATTAATGAATCGGCCAAACGCGCGGAGAGCGGTTTGCATTTGGCGCTCTTC	10224	GGGTGGCGCAAGAACTCCAGCATGAGATCCCGCGCTGGAGGATCATCCAGCCGCGTC	10283
QY	2946	CGCTTCCCTCGCTCACTGACTCGCTCGCTCGCTCGCTCGCTCGCGCGAGCGGTATCAGC	4026	CCGAAAAACGATTCGGAAGCCCAACCTTTTCATAGAAGCGCGGTGGAAATCGAAATCTCG	4085
Db	9348	CGCTTCCCTCGCTCACTGACTCGCTCGCTCGCTCGCTCGCTCGCGCGAGCGGTATCAGC	10284	CCGAAAAACGATTCGGAAGCCCAACCTTTTCATAGAAGCGCGGTGGAAATCGAAATCTCG	10343
QY	3006	TCACTCAAAGCGGTAAATAGGTTATCCACAGATCAGGGGATAAGCGAGGAAGACAT	4086	TGATGGCAGGTTGGCGCTCGCTTGGTTCGATTTTCGAACCCACAGTCCCGCTCAGAAG	4145
Db	9408	TCACTCAAAGCGGTAAATAGGTTATCCACAGATCAGGGGATAAGCGAGGAAGACAT	10344	TGATGGCAGGTTGGCGCTCGCTTGGTTCGATTTTCGAACCCACAGTCCCGCTCAGAAG	10403
QY	3066	GTGAGCAAAAGGCCAGCAAGGCCAGGAACCGTAAAGGCGCGCTTCTCGCGTTTTT	4146	AACTCGTCAAGAGCGATAGAAGCGGATGCGCTCGAATCGGGAGCGCGATACCGTAA	4205
Db	9468	GTGAGCAAAAGGCCAGCAAGGCCAGGAACCGTAAAGGCGCGCTTCTCGCGTTTTT	10404	AACTCGTCAAGAGCGATAGAAGCGGATGCGCTCGAATCGGGAGCGCGATACCGTAA	10463
QY	3126	CCATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCAGACGCTCAAGTCAGAGTGGCG	4206	AGCAGAGGAAGCGGTACGCCCATTTGCGCGCCAGCTCTTCAGCAATATCACGGGTAGCC	4265
Db	9528	CCATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCAGACGCTCAAGTCAGAGTGGCG	10464	AGCAGAGGAAGCGGTACGCCCATTTGCGCGCCAGCTCTTCAGCAATATCACGGGTAGCC	10523
QY	3186	AAACCCGACAGACTATAAGATACAGGCGTTTCCCGCTGGAAGCTCCCTCGTGGCTC	4266	AACTGATGTCCTGATAGCGGTCCGCCACACCCAGCCGCGCACAGTCGATGAATCCAGAA	4325
Db	9588	AAACCCGACAGACTATAAGATACAGGCGTTTCCCGCTGGAAGCTCCCTCGTGGCTC	10524	AACTGATGTCCTGATAGCGGTCCGCCACACCCAGCCGCGCACAGTCGATGAATCCAGAA	10583
QY	3246	TCTGTTTCCGACCTCGCTTACCGGATACCTGTCGCGCTTCTCCCTTCGGGAAGCGT	4326	AACTGATGTCCTGATAGCGGTCCGCCACACCCAGCCGCGCACAGTCGATGAATCCAGAA	4385
Db	9648	TCTGTTTCCGACCTCGCTTACCGGATACCTGTCGCGCTTCTCCCTTCGGGAAGCGT	10584	AACTGATGTCCTGATAGCGGTCCGCCACACCCAGCCGCGCACAGTCGATGAATCCAGAA	10643
QY	3306	GGCGCTTCTCAATGCTCAGCTGTAGGTATCTCAGTTCGGTGTAGGTTCGCTCCAA	4386	TCCTCGCGTTCGGGATCGCGCTTGAAGCTGGGCAACAGTTCGGCTGGCGCGAGCCCC	4445
Db	9708	GGCGCTTCTCAATGCTCAGCTGTAGGTATCTCAGTTCGGTGTAGGTTCGCTCCAA	10644	TCCTCGCGTTCGGGATCGCGCTTGAAGCTGGGCAACAGTTCGGCTGGCGCGAGCCCC	10703
QY	3366	GCTGGGCTGTGTCAGAAACCCCGCTTACGCGGACCGCTGCGCTTATTCGGTAACTA	4446	TGATGCTCTTCTGTCAGATCATCTGATCGACAAGCCGCTTCCATCGAGTACGTGT	4505
Db	9768	GCTGGGCTGTGTCAGAAACCCCGCTTACGCGGACCGCTGCGCTTATTCGGTAACTA	10704	TGATGCTCTTCTGTCAGATCATCTGATCGACAAGCCGCTTCCATCGAGTACGTGT	10763
QY	3426	TGCTTTGAGTCCAAACCCCGTAAAGACAGCACTTATCGCACTGGCAGCAGCACTGGTAA	4506	CGCTCGATGCGATGTTTCGCTTGGTGTGTAATGGGCGAGGTAGCCGATCAAGCGTATGC	4565
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QY	3486	CAGGATTTAGCAGAGCAGGTATGAGCGGTGCTACAGAGTTCTTGAAGTGGTGGCTAA	4566	AGCCCGCGATTTGATCAGCCATGATGGATACCTTCTCGGAGGAGCAAGGTGAGTGC	4625
Db	9888	CAGGATTTAGCAGAGCAGGTATGAGCGGTGCTACAGAGTTCTTGAAGTGGTGGCTAA	10824	AGCCCGCGATTTGATCAGCCATGATGGATACCTTCTCGGAGGAGCAAGGTGAGTGC	10883
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Db	9948	CTACGGCTACCTAGAGAACAGTATTTGGTATCTCGGCTCTGCTGAAGCCAGTTACCTT	4686	AGCTCGAGCACAGCTCGCAAGAAACGCCCGCTGCTGGCCAGCCAGTAGCCGCGTGC	4745
QY	3606	CGGAAAAAGTTGGTAGCTCTTGTATCCGCAAAACAAACACCGCTGGTAGCGTGGTTT	10944	ACGTCGAGCACAGCTGCGCAAGAAACGCCCGCTGCTGGCCAGCCAGTAGCCGCGTGC	11003
Db	10008	CGGAAAAAGTTGGTAGCTCTTGTATCCGCAAAACAAACACCGCTGGTAGCGTGGTTT	4746	TGCTCCTGAGTTCAATTCAGGCGACCGGACAGGTTCGTTGCAAAAAAGAACCCGGCGC	4805
QY	3666	TTTTTTTGAACAGCAGATTAACGCGCAAAAAAAGGATCTCAAGAAAGATCTTTGTAT	11004	TGCTCCTGAGTTCAATTCAGGCGACCGGACAGGTTCGTTGCAAAAAAGAACCCGGCGC	11063
Db	10068	TTTTTTTGAACAGCAGATTAACGCGCAAAAAAAGGATCTCAAGAAAGATCTTTGTAT	4806	CCCTCGCTGACAGCCGGAACACCGCGCATCAGAGCAGCCGATTTGTTGTGCCAG	4865
QY	3726	CTTTTCTACGGGCTCTGACGCTCAGTGGAAACGAAACTCAGTTAAGGATTTTGTGAT	11064	CCCTCGCTGACAGCCGGAACACCGCGCATCAGAGCAGCCGATTTGTTGTGCCAG	11123
Db	10128	CTTTTCTACGGGCTCTGACGCTCAGTGGAAACGAAACTCAGTTAAGGATTTTGTGAT	4866	TCATAGCCGAATPAGCTCTTCCACCAAGCGCGGAGAACTTCGCTGCAATCCATCTTGT	4925
QY	3786	GAGATTATCGTCACCAAGCGGCCATCGTGCCTCCCACTCTCTCGAGTTCGGGGGCATG	11124	TCATAGCCGAATPAGCTCTTCCACCAAGCGCGGAGAACTTCGCTGCAATCCATCTTGT	11183

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Qy 4926 TCAATCATGCGAAACGATCCCTCATCTGCTCTTTGATCAGATCTTGTATCCCTCGGCGCAT 4985
Db 11184 TCAATCATGCGAAACGATCCCTCATCTGCTCTTTGATCAGATCTTGTATCCCTCGGCGCAT 11243
Qy 4986 CAGATCTTGGCGGCAAGAACGATCCAGTCTTCTTGGAGGCTTCCCAACCTTACCA 5045
Db 11244 CAGATCTTGGCGGCAAGAACGATCCAGTCTTCTTGGAGGCTTCCCAACCTTACCA 11303
Qy 5046 GAGGGCGCCCGAGCTGGCAATTCGGGTTCCGCTTGTCTGCTCCATAAAACCGCCAGTCTAGC 5105
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Qy 5106 TATCGCCATGTAAGCCCACTGCAAGTACTGCTTCTTTGGCGTGTGGTTTCCCTT 5165
Db 11364 TATCGCCATGTAAGCCCACTGCAAGTACTGCTTCTTTGGCGTGTGGTTTCCCTT 11423
Qy 5166 GTCCAGATAGCCAGTAGCTGACATTCATCCGGGCTCAGCACCGTTTCTCGGACCTGGCT 5225
Db 11424 GTCCAGATAGCCAGTAGCTGACATTCATCCGGGCTCAGCACCGTTTCTCGGACCTGGCT 11483
Qy 5226 TTCTAGCTGTTCCGCTTCTTCTTAGCAGCCCTTGGCCCTCAGTGTCTTGGCGAGCGTG 5283
Db 11484 TTCTAGCTGTTCCGCTTCTTCTTAGCAGCCCTTGGCCCTCAGTGTCTTGGCGAGCGTG 11541

RESULT 4
US-10-322-360-1/c
; Sequence 1, Application US/10322360
; Publication No. US20030165946A1
; GENERAL INFORMATION:
; APPLICANT: Evans, Glen A.
; TITLE OF INVENTION: A Method for the Complete Chemical
; TITLE OF INVENTION: Synthesis and Assembly of Genes and Genomes
; FILE REFERENCE: P-EA 5511
; CURRENT APPLICATION NUMBER: US/10/322,360
; CURRENT FILING DATE: 2002-12-17
; PRIOR APPLICATION NUMBER: US 09/554,929
; PRIOR FILING DATE: 2000-05-12
; NUMBER OF SEQ ID NOS: 193
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 4800
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic plasmid
US-10-322-360-1

Query Match 33.9%; Score 1793.4; DB 16; Length 4800;
Best Local Similarity 91.8%; Pred. No. 0;
Matches 1980; Conservative 0; Mismatches 1; Indels 176; Gaps 1;

Qy 3127 CATAGGCTCGCCCCCTGACGAGCATCAAAAATCGACGCTCAAGTCAGAGGTGGCGA 3186
Db 4800 CATAGGCTCGCCCCCTGACGAGCATCAAAAATCGACGCTCAAGTCAGAGGTGGCGA 4741
Qy 3187 AACCCGACAGGACTAAAGATACACGAGGCTTCCCGCTGGAGCTCCCTCGTGGCTCT 3246
Db 4740 AACCCGACAGGACTAAAGATACACGAGGCTTCCCGCTGGAGCTCCCTCGTGGCTCT 4681
Qy 3247 CTTGTTCCGACCTCGCGCTTACCGGATACCTGTCCGCTTCTCCCTTCGGGAAGCGTG 3306
Db 4680 CTTGTTCCGACCTCGCGCTTACCGGATACCTGTCCGCTTCTCCCTTCGGGAAGCGTG 4621
Qy 3307 GCCTTTCTCATAGCTCAGCTAGGTACTCAGTTCCGTTCCGTTCCGTTCCGTTCCGTT 3366
Db 4620 GCCTTTCTCATAGCTCAGCTAGGTACTCAGTTCCGTTCCGTTCCGTTCCGTTCCGTT 4561
Qy 3367 CTGGGCTGTGCAAGAACCCCGCTTCCGCGAGCGCTGCGCTTATCCGTTACTAT 3426
Db 4560 CTGGGCTGTGCAAGAACCCCGCTTCCGCGAGCGCTGCGCTTATCCGTTACTAT 4501
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Qy 3427 CGTCTTGAFTCCAAACCCGGTAAGACACGACTTATCCCACTGGCAGCAGCCACTGGTAAC 3486
Db 4500 CGTCTTGAFTCCAAACCCGGTAAGACACGACTTATCCCACTGGCAGCAGCCACTGGTAAC 4441
Qy 3487 AGGATTTAGCAGCAGGAGTATGTAGCGGTGCTACAGAGTTCTTTGAAGTGGTGGCCTAAC 3546
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Qy 3607 GGAAGAAAGTGGTGTAGCTCTTGTATCCGGCAAAACAAACCAACCGCTGGTACGGTGGTTT 3666
Db 4320 GGAAGAAAGTGGTGTAGCTCTTGTATCCGGCAAAACAAACCAACCGCTGGTACGGTGGTTT 4261
Qy 3667 TTTGTTTGAACGAGCAGGATTAAGCGCAGAAAAAAGGATCTCAAGAAATCCTTTGATC 3726
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Qy 3967 GGGTGGCGAAGAACTCCAGCATGAGATCCCGCGCTGGAGGATCATCCAGCGCGGTCC 4026
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Qy 4027 CGGAAAAAGATTCCGAAGCCCAACCTTTTATAGAGGCGCGGTGGAATCGAAATCTCGT 4086
Db 4076 CGGAAAAAGATTCCGAAGCCCAACCTTTTATAGAGAGCGCGGTGGAATCGAAATCTCGT 4017
Qy 4087 GATGCGAGGTTGGGCGTCTTGGTCTGCTTTCGAAACCCAGAGTCCCGCTCAGAGA 4146
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Qy 4447 GATGCTCTTGGTCCAGATCATCTGATCGAAGAACCGGCTTCCATCCGAGTACGTC 4506
Db 3656 GATGCTCTTGGTCCAGATCATCTGATCGAAGAACCGGCTTCCATCCGAGTACGTC 3597
Qy 4507 GCTCGATGCGATGTTTTCGCTTGGTGGTGGAGTAGTAGCCGATCAAGCGTAGTGA 4566
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Db 3596 GCTCGATGCGATGTTTCGCTTGGTGTGATGGGAGGTAGCGGATCAAGCGTATGCA 3537
QY 4567 GCGCGCGATGTCATCAGCCATGATGATGATCTTTCTCGCAGAGAGCAAGGTGAGATGACA 4626
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Db 3476 GGAGATCCTGCGCCGCGCATCTCGCCCAATAGCAGCGAGTCCCTTCGCGCTTCAGTGACAA 3417
QY 4687 CBTGCGAGCAGCTGCGCAGGAACCGCCGCTCGTGGCCAGCCACGATAGCCGCGCTGCGCT 4746
Db 3416 CBTGCGAGCAGCTGCGCAGGAACCGCCGCTCGTGGCCAGCCACGATAGCCGCGCTGCGCT 3357
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QY 4927 CAATCATGCGAAACGATCTCTATCTCTGTCATGATCAGATCTTGATCCCTCGCGCATC 4986
Db 3176 CAATCATGCGAAACGATCTCTATCTCTGTCATGATCAGATCTTGATCCCTCGCGCATC 3117
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Db 3116 AGATCCTTGGCGCAGAAAGCCATCCAGTTTACTTTGAGGGCTTCCCAACCTTACCAG 3057
QY 5047 AGGCGCGCCAGCTGCGCAATTCGGTTCGCTGTCATATAAACCGCCAGCTTAGCT 5106
Db 3056 AGGCGCGCCAGCTGCGCAATTCGGTTCGCTGTCATATAAACCGCCAGCTTAGCT 2997
QY 5107 ATGCGCATGTAAGCCCACTGCAAGCTACTGCTTTCTTTGGCGCTTGCTTTCCCTTG 5166
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QY 5167 TCCAGATAGCCAGTAGCTGACATTCATCCGGGTGAGCAGCCGCTTTCGGGAGCTGGCT 5226
Db 2936 TCCAGATAGCCAGTAGCTGACATTCATCCGGGTGAGCAGCCGCTTTCGGGAGCTGGCT 2877
QY 5227 TCTACGTGTTCCGCTTCCCTTTAGCAGCCCTTGGCGCCCTGAGTGCCTTTCGGGAGCTGG 5283
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RESULT 5
US-10-811-028A-5
; Sequence 5, Application US/10811028A
; Publication No. US20050043258A1
; GENERAL INFORMATION:
; APPLICANT: Bennett, Michael
; APPLICANT: Chen, Yen-Ju
; APPLICANT: Genteric, Inc.
; TITLE OF INVENTION: Methods of Treating Xerostomia and Xerophthalmia
; FILE REFERENCE: 020714-002410US
; CURRENT APPLICATION NUMBER: US/10/811,028A
; CURRENT FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: US 60/458,793
; PRIOR FILING DATE: 2003-03-26
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 4058
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence:pMB1-hIPN-alpha
; OTHER INFORMATION: plasmid expression vector
US-10-811-028A-5
Query Match 32.1%; Score 1697.8; DB 21; Length 4058;
Best Local Similarity 86.7%; Pred. No. 0;
Matches 1980; Conservative 0; Mismatches 102; Indels 201; Gaps 2;
QY 2706 CTAGACGTAATCATGGTCTATAGCTGTTTCTGTTGTAATTTGTTATCCGCTCACAAATCC 2765
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Db 2037 ACACAAACATACGAGCGGGAAGCATAAAGTGTAAAGCCTGGGGTGCTTAATGAGTGAGCTA 2096
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Db 2157 GCTGCATTAATGAATTCGGCCCAACCGCGGGGAGAGCGGTTTGGTATTTGGCGCTCTTC 2216
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QY 3126 CCATAGGCTTCGCGCCCTCGAGCAGCATCACAAAAATCGACCTCAAGTCAGAGTGGCG 3185
Db 2397 CCATAGGCTTCGCGCCCTCGAGCAGCATCACAAAAATCGACCTCAAGTCAGAGTGGCG 2456
QY 3186 AAACCCGACAGGACTATAAAGATACAGCGGTTTCCCTGGAAGCTCCCTCGTGGGCTC 3245
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Db 2577 GCGCGCTTTCCTCATAGCTCACTGCTGAGGTATCTCAGTTTCGGGTGAGTGCCTTCGCTCCAA 2636
QY 3366 GCTGGGCTGTGTCACGAAACCCCGCTTCAGCCGAGCGCTCGCGCTTATCCGGTAACCTA 3425
Db 2637 GCTGGGCTGTGTCACGAAACCCCGCTTCAGCCGAGCGCTCGCGCTTATCCGGTAACCTA 2696
QY 3426 TCGCTTTCAGTCAACCCCGGTAAGACAGCTTATCGCCACTGCGAGCGACCTGGTAA 3485
Db 2697 TCGCTTTCAGTCAACCCCGGTAAGACAGCTTATCGCCACTGCGAGCGACCTGGTAA 2756
QY 3486 CAGGATTAAGCAGGAGGTATGAGGCGGTCTACTACAGAGTTCTTGAAGTGTGGCGCTAA 3545
Db 2757 CAGGATTAAGCAGGAGGTATGAGGCGGTCTACTACAGAGTTCTTGAAGTGTGGCGCTAA 2816
QY 3546 CTACGCGTACACTAGAAGAACAGTATTTGGTATCTCGGCTCTGCTGAAGCCAGTTACCTT 3605
Db 2817 CTACGCGTACACTAGAAGAACAGTATTTGGTATCTCGGCTCTGCTGAAGCCAGTTACCTT 2876
QY 3606 CGGAAAGAGTTGGTAGCTCTTGATCCGGCAAAACAAACCCGCTGGTGGAGCGGTGTTT 3665
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QY 3666 TTTTGTTCGAAGCAGCAGATTTACGCGCAGAAAAAAGGATCTCAAGAGAGATCTCTTTGAT 3725

	Db	2937	 TTTTGTTGCAAGCAGCAGATTACGCCAGAAAAAAGGATCTCAAGAAGATCCTTTGAT
	Qy	3726	CTTTCCTACGGGGTCTCAGCGCTCAGTGGAACCAAAAATCACGTTTAAGGATTTTGGTGCAT
	Db	2997	CTTTCCTACGGGGTCTCAGCGCTCAGTGGAACCAAAAATCACGTTTAAGGATTTTGGTGCAT
	Qy	3786	GAGANTATCGTCGACAAGCGGCCATCGTGTCCCTCCCACACTCTCTGCAgTTTCGGGGGGCATG
	Db	3057	 GAG
	Qy	3846	GATGCGCGGATAGCGGCTGCTGGTTCCTCGATGCGCAGCGATTGTCACCTGCCGGTAGAA
	Db	3060	-----
	Qy	3906	CTCCGCGAGGTCGTCCAGCGCTCAGGCAGCAGCTGAACCAACTCGCAGGGGATCGAGCCC
	Db	3060	-----CGGATACATAATTGNATGTTATTAGAAAAATAACAATAG
	Qy	3966	GGGGTGGCGAAGAACCTCCAGCATGAGATCCCCGGCTGGAGGATCATCAGCGCGGCTC
	Db	3101	 GGGTTCCGCGCACAATTTCCCGAAAAAGTGCCACCCTGTATGCGGTGCAAAATACCGCACAG
	Qy	4026	CCGGAACCAATCCGAAAGCCCAACTTTTATAGAAGCGCGGTGGAATCGAAATCTCG
	Db	3161	 ATCGGTAAGAGAGAAAATACCGCATCAGGAAATTTGTAAGCGTTAATAAT-
	Qy	4086	TGATGGCAGGTTGGCGCTCGTTGGTCGGTCAATTTCCGAACCCACAGAGTCCCGCTCAGAAG
	Db	3209	-----TCAGAG
	Qy	4146	AATCTGTTCAAAGAGCGGATAGAAGCGGATGCGTTCGAAATCGGAGCGGGATACCGTAA
	Db	3216	AATCTGTTCAAAGAGCGGATAGAAGCGGATGCGTTCGAAATCGGAGCGGGATACCGTAA
	Qy	4206	AGCACAGGAAGCGGTCAGGCCCATTCGCCGCCAAGCTCTTCAGCAATATCACGGGTAGCC
	Db	3276	AGCACAGGAAGCGGTCAGGCCCATTCGCCGCCAAGCTCTTCAGCAATATCACGGGTAGCC
	Qy	4266	AACGCTATGTCCTGATAGCGGTCCGCCACACCACCGCGGCACAGTCGATGAAATCCAGAA
	Db	3336	AALGCTATGTCCTGATAGCGGTCCGCCACACCACCGCGGCACAGTCGATGAAATCCAGAA
	Qy	4326	AAGCGGCCAATTTCCACCATGATATTCGGCAAGCAGGCATCGCATGGGTACGACGAGA
	Db	3396	AAGCGGCCAATTTCCACCATGATATTCGGCAAGCAGGCATCGCATGGGTACGACGAGA
	Qy	4386	TCCTCGCGTTCGGGCATCGCGGCTTGAGCTGGCGAACAAGTTTCGGTTCGGTGGCGAGCCCC
	Db	3456	TCCTCGCGTTCGGGCATCGCTCGCTTCGGCGAACAAGTTTCGGTTCGGTGGCGAGCCCC
	Qy	4446	TGATGCTCTTCGTCAGATCATCTGATCCACAAGACCGGCTTCCTCCAGTACGTTGCT
	Db	3516	TGATGCTCTTCGTCAGATCATCTGATCCACAAGACCGGCTTCCTCCAGTACGTTGCT
	Qy	4506	CGCTCGATGCGATGTTTCGCTTGGTGGTCCAATGGGCAAGTACGCCGATCAAGCGTATGC
	Db	3576	CGCTCGATGCGATGTTTCGCTTGGTGGTCCAATGGGCAAGTACGCCGATCAAGCGTATGC
	Qy	4566	AGCCGCGCANNTGCATCAGCCATGATGGATACCTTTCTCGGCAAGGACAAGGTGAGATGAC
	Db	3636	AGCCGCGCANNTGCATCAGCCATGATGGATACCTTTCTCGGCAAGGACAAGGTGAGATGAC
	Qy	4626	AGGAGATCTCGCCCCCGCACTTCGCCCAATAGCAGCCAGTCCCTTCCTCCGTTTCAGTTGACA
	Db	3696	AGGAGATCTTCGCCCCCGGCACTTCGCCCAATAGCAGCCAGTCCCTTCCTCCGTTTCAGTTGACA
	Qy	4686	ACGTCGAGCACAGCTGGCAAGGAAACGCCCGCTCGTGGCCAGCAACGATACCCCGGTGCC
	Db	3756	ACGTCGAGCACAGCTGGCAAGGAAACGCCCGCTCGTGGCCAGCAACGATACCCCGGTGCC
	Qy	4746	TCGTCCTGCAGTTCAATTCAGGGCACCGGACAGGTCGGTCTTTGACAAAAGAAACCGGGCGC

Db	3816	TCGTCTTTCAGTTTCATTTCAGGGCACCCGGACAGGTCGGTCTTTGACAAAAGAAACCGGGCGC	3875
Qy	4806	CCCTGGCGTGCACAGCCGGAAACACGGGGGCATCAGAGCAGCCGATTGTCCTTCTGTCGCCAG	4865
Db	3876	CCCTGGCGTGCACAGCCGGAAACACGGGGGCATCAGAGCAGCCGATTGTCCTTCTGTCGCCAG	3935
Qy	4866	TCATAGCCGAATAGCCTCTCCACCCAAAGCGCCGGAGAACCTCGTCGCAATCCATCTTGT	4925
Db	3936	TCATAGCCGAATAGCCTCTCCACCCAAAGCGCCGGAGAACCTCGTCGCAATCCATCTTGT	3995
Qy	4926	TCAATCATGCGAAGCATCTCATCTCTCTCTTGTATCAGATCTTGATCCCTTGCGCCAT	4985
Db	3996	TCAATCATGCGAAGCATCTCATCTCTCTCTTGTATCAGAGCTTGATCCCTTGCGCCAT	4055
Qy	4986	CAG 4988	
Db	4056	CAG 4058	
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US-10-811-028A-6			
; Sequence 6, Application US/10811028A			
; Publication No. US20050043258A1			
; GENERAL INFORMATION:			
; APPLICANT: Bennett, Michael			
; APPLICANT: Chen, Yen-Ju			
; APPLICANT: Gentric, Inc.			
; TITLE OF INVENTION: Methods of Treating Xerostomia and Xerophthalmia			
; FILE REFERENCE: 020714-002410US			
; CURRENT APPLICATION NUMBER: US/10/811,028A			
; CURRENT FILING DATE: 2004-03-25			
; PRIOR APPLICATION NUMBER: US 60/458,793			
; PRIOR FILING DATE: 2003-03-26			
; NUMBER OF SEQ ID NOS: 11			
; SOFTWARE: PatentIn Ver. 2.1			
; SEQ ID NO 6			
; LENGTH: 4187			
; TYPE: DNA			
; ORGANISM: Artificial Sequence			
; FEATURE:			
; OTHER INFORMATION: Description of Artificial Sequence:pWB1-EcsOD			
; OTHER INFORMATION: plasmid expression vector			
US-10-811-028A-6			
Query Match 32.1%; Score 1697.8; DB 21; Length 4187;			
Best_Local Similarity 86.7%; Pred.No. 0;			
Matches 1980; Conservative 0; Mismatches 102; Indels 201; Gaps 2;			
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Db	2106	CTTGGCGTAATCATGGTCATAGCTGTTTCTCTGTGTGAAATTTGTTATTCGCTCACAAATCC	2165
Qy	2766	ACACAATACAGAGCCGGAGACATAAGTGTAAAGCCTGGGTGCCTAATAGTGAAGCTA	2825
Db	2166	ACACAATACAGAGCCGGAGACATAAGTGTAAAGCCTGGGTGCCTAATAGTGAAGCTA	2225
Qy	2826	ACTCACATTAATTCGTTGGCGTCACTGCGCGCTTTCACAGTCGGGAAACCTGTCGTCGCA	2885
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Qy	2886	GCTGCATTAATGAATCGGCCAACCGCGGGGAGAGCGGTTTCGTTATTTGGCGCTCTTC	2945
Db	2286	GCTGCATTAATGAATCGGCCAACCGCGGGGAGAGCGGTTTCGTTATTTGGCGCTCTTC	2345
Qy	2946	CGCTTCCTCGCTCACTGACTCGTTCGTCGCTCGGTCGTTTCGCGTCGCGCGAGCGGTATCAGC	3005
Db	2346	CGCTTCCTCGCTCACTGACTCGTTCGTCGCTCGGTCGTTTCGCGTCGCGCGAGCGGTATCAGC	2405
Qy	3006	TCACTCAAGGCGGTAAACGGTTATCCACAGAAATCAGGGGATACGCGAGGAAGCAAT	3065
Db	2406	TCACTCAAGGCGGTAAACGGTTATCCACAGAAATCAGGGGATACGCGAGGAAGCAAT	2465
Qy	3066	GTGAGCAAAAGGCCAGCAAAAGGCCAGGAAACCGTAAAAAGGCCGGCTTGCTGGCGCTTTT	3125

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2526 CCATAGGCTCCGCCCTTGACGAGCATCAAAAAATCAAGTCAAGGTGGCG 2585
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3246 TCCTGTTCCGACCTCCGCTTACCGGATACCTGTCGCGCTTCTCCCTCGGAGCGT 3305
Db
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3306 GGCGCTTTCTCATAGCTCAGCTGTAGTATCTCAGTTCGGTGTAGTGTCTCGCTCCAA 3365
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Db
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3066 TTTTGTGTTGCAAGCAGCAGATTACGCGCAAAAAAGGATCTCAAGAAAGATCCTTTGAT 3125
QY
3726 CTTTTCTACGGGTCTGACGCTCAGTGGAACGAAATCTACGTTAAGGATTTTGTGCTAT 3785
Db
3126 CTTTTCTACGGGTCTGACGCTCAGTGGAACGAAATCTACGTTAAGGATTTTGTGCTAT 3185
QY
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3186 GAG----- 3188
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3846 GATGCGGGATAGCCGCTGCTGTTTCTGGATGCGGACGGATTTGCACTGCGCGTAGAA 3905
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3189 ----- 3188
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3189 -----CGGATACATATTTGAATGTTATTAGAAAAATAAACAATAAG 3229
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Db
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Db
3405 AGCAGAGGAAGCGGTAGCCCATTCGCGCGCAAGCTTTTCAGCAATATCACGGTAGCC 3464
QY
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4326 AAGCGCCATTTTCCACCATGATATTTCGCAAGCAGGAGCATCGCCATGGGTCAACAGCAGA 4385
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RESULT 7

US-10-811-028A-2

; Sequence 2, Application US/10811028A

; Publication No. US20050043258A1

; GENERAL INFORMATION:

; APPLICANT: Bennett, Michael

; APPLICANT: Chen, Yen-Ju

; APPLICANT: Genteric, Inc.

; TITLE OF INVENTION: Methods of Treating Xerostomia and Xerophthalmia

; FILE REFERENCE: 020714-002410US

; CURRENT APPLICATION NUMBER: US/10/811,028A

; CURRENT FILING DATE: 2004-03-25

; PRIOR APPLICATION NUMBER: US 60/458,793

; PRIOR FILING DATE: 2003-03-26

NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4293
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: pMB1-HAMsOD
; OTHER INFORMATION: plasmid expression vector
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (1940)
; OTHER INFORMATION: n = g, a, c or t
US-10-811-028A-2

Query Match 32.1%; Score 1697.8; DB 21; Length 4293;
Best Local Similarity 86.7%; Pred. No. 0;
Matches 1980; Conservative 0; Mismatches 102; Indels 201; Gaps 2;

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DB 2272 ACACAAATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTCCCTAATGAGTGACTA 2331

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DB 2332 ACTCACATTAATTCGGTTCGCTCAGTCCGCTTCCAGTCCGGGAACCTGTCGCCA 2391

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QY 4566 AGCCGCGCATTCGATCAGCCATGATGATATCTTTCTCGGCGAGGAGCAAGGTGAGATGAC 4625
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Db |||||
QY 3730 TCCTCGCGCTGGGCGATCGCTGCGCTTGAGCTGGCGAAAGATTCGCGTGGCGGAGCGGCC 3789
QY 4446 TGATGCTCTTTCGTCAGATCATCTGATCGACAGACCGGCTTCATCCGAGTACGTGCT 4505
Db |||||
QY 3790 TGATGCTCTTTCGTCAGATCATCTGATCGACAGACCGGCTTCATCCGAGTACGTGCT 3849
QY 4506 CGCTCGATGCGATGTTTTCGCTTGGTTCGAATGGGCGAGGTAGCCGATCAACGCGTATGC 4565
Db |||||
QY 3850 CGCTCGATGCGATGTTTTCGCTTGGTTCGAATGGGCGAGGTAGCCGATCAACGCGTATGC 3909
QY 4566 AGCGCGCGATTCGATCAGCATGATGATGATCTTTCTCGGCGAGGAGCAAGGTGAGATGAC 4625
Db |||||
QY 3910 AGCGCGCGATTCGATCAGCATGATGATGATCTTTCTCGGCGAGGAGCAAGGTGAGATGAC 3969
QY 4626 AGGAGATCTGCGCCGCACTTCGCGCAATAGCAGCGAGTCCCTTCGCGCTTCAGTGACA 4685
Db |||||
QY 3970 AGGAGATCTGCGCCGCACTTCGCGCAATAGCAGCGAGTCCCTTCGCGCTTCAGTGACA 4029
QY 4686 ACCTCGAGCAGCTGCGCAAGGAAGCGCCGCTGCTGGCCAGCCAGCATAGCCGCGTGC 4745
Db |||||
QY 4030 ACCTCGAGCAGCTGCGCAAGGAAGCGCCGCTGCTGGCCAGCCAGCATAGCCGCGTGC 4089
QY 4746 TCGTCTGCAAGTTTCAATTCAGGCAACCGGACAGGTCTGTGACAAAGAAACCGGCGC 4805
Db |||||
QY 4090 TCGTCTGCAAGTTTCAATTCAGGCAACCGGACAGGTCTGTGACAAAGAAACCGGCGC 4149
QY 4806 CCCTGCGCTGACAGCGGACAGCGGCGCATCAGCGCGGATCTGCTGTTGCGCCAG 4865
Db |||||
QY 4150 CCCTGCGCTGACAGCGGAAACAGCGGCGCATCAGCGCGGATGCTGTTGTTGCGCCAG 4209
QY 4866 TCATAGCCGAATAGCTCTCCACCCCAAGCGCGCGGAGAACCTCGCTGCAATCATCTTGT 4925
Db |||||
QY 4210 TCATAGCCGAATAGCTCTCCACCCCAAGCGCGCGGAGAACCTCGCTGCAATCATCTTGT 4269
QY 4926 TCAATCATGCGAAACGATCTCATCTCTTGTCTTGTATCAGATCTTGTATCCCTTCGCCAT 4985
Db |||||
QY 4270 TCAATCATGCGAAACGATCTCATCTCTTGTCTTGTATCAGATCTTGTATCCCTTCGCCAT 4329
QY 4986 CAG 4988
Db |||||
QY 4330 CAG 4332
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RESULT 9

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US-10-811-028A-3
; Sequence 3, Application US/10811028A
; Publication No. US20050043258A1
; GENERAL INFORMATION:
; APPLICANT: Bennett, Michael
; APPLICANT: Chen, Yen-Ju
; APPLICANT: Genteric, Inc.
; TITLE OF INVENTION: Methods of Treating Xerostomia and Xerophthalmia
; FILE REFERENCE: 020714-002410US
; CURRENT APPLICATION NUMBER: US/10/811,028A
; CURRENT FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: US 60/458,793
; PRIOR FILING DATE: 2003-03-26
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; TYPE: DNA
; LENGTH: 5753
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:pMB1-CAT
; OTHER INFORMATION: plasmid expression vector
US-10-811-028A-3
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Query Match 32.1%; Score 1697.8; DB 21; Length 5753;
Best Local Similarity 86.7%; Pred. No. 0;
Matches 1980; Conservative 0; Mismatches 102; Indels 201; Gaps 2;

QY 2706 CTAGACGTAATCATGTCTATAGTGTTCCTCTGTGTGAAATTTGTTATCCGCTCACAATTC 2765
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QY 3672 CTTGGCGTAATCATGTCTATAGTGTTCCTCTGTGTGAAATTTGTTATCCGCTCACAATTC 3731
Db |||||
QY 2766 ACACACATACAGCGCGGAAGCATAAAGTGTAAAGCTGGGTCCTTAATGATGAGCTA 2825
Db |||||
QY 3732 ACACACATACAGCGCGGAAGCATAAAGTGTAAAGCTGGGTCCTTAATGATGAGCTA 3791
Db |||||
QY 2826 ACTCACATTAATTTGGCTTCGCTCTACTGCGCGCTTTCAGTCGGGAAACCTGTCGCGCA 2885
Db |||||
QY 3792 ACTCACATTAATTTGGCTTCGCTCTACTGCGCGCTTTCAGTCGGGAAACCTGTCGCGCA 3851
Db |||||
QY 2886 GCTGCATTAATGAATCGGCCAACCGCGCGGAGAGCGGTTTCGCTATTGGGCGCTCTTC 2945
Db |||||
QY 3852 GCTGCATTAATGAATCGGCCAACCGCGCGGAGAGCGGTTTCGCTATTGGGCGCTCTTC 3911
QY 2946 CGCTTCCTCGCTCACTGACTCGCTGCGCTCGCTGCGCTGCGGCGAGCGGTATCAGC 3005
Db |||||
QY 3912 CGCTTCCTCGCTCACTGACTCGCTGCGCTCGCTGCGCTGCGGCGAGCGGTATCAGC 3971
QY 3006 TCACTCAAAGCGGTAATACGGTTATCCACAGATCAGGGGATACCGAGGAAAGAACAT 3065
Db |||||
QY 3972 TCACTCAAAGCGGTAATACGGTTATCCACAGATCAGGGGATACCGAGGAAAGAACAT 4031
QY 3066 GTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCGCGTTGCTGCGGTTTTT 3125
Db |||||
QY 4032 GTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCGCGTTGCTGCGGTTTTT 4091
QY 3126 CCATAGGCTTCGCGCCCTTCGACGAGCATCAAAAATCAGACGCTCAAGTCAGAGTGGCG 3185
Db |||||
QY 4092 CCATAGGCTTCGCGCCCTTCGACGAGCATCAAAAATCAGACGCTCAAGTCAGAGTGGCG 4151
QY 3186 AAACCCGACAGGACTATAAGATACAGGCGTTTCCCTGGAAGCTCCCTCGTCGCTC 3245
Db |||||
QY 4152 AAACCCGACAGGACTATAAGATACAGGCGTTTCCCTGGAAGCTCCCTCGTCGCTC 4211
QY 3246 TCTGTTCCGACCCCTCGCTTACCGGATACCTGTCGCGCTTTCTCCCTTCGGGAAGCGT 3305
Db |||||
QY 4212 TCTGTTCCGACCCCTCGCTTACCGGATACCTGTCGCGCTTTCTCCCTTCGGGAAGCGT 4271
QY 3306 GCGGCTTTCTCATAGCTACGCTGATAGGTATCTCAGTTCCGTTGATGCTTCGCTCCAA 3365
Db |||||
QY 4272 GCGGCTTTCTCATAGCTACGCTGATAGGTATCTCAGTTCCGTTGATGCTTCGCTCCAA 4331
Db |||||
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QY	4446	TGATGCTCTTCGTCCAGATCATCTGTATCGACAAGACCGGCTTCCATCCAGGTACGTGCT	4505
Db	5211	TGATGCTCTTTCGTCCAGATCATCTGTATCGACAAGACCGGCTTCCATCCAGGTACGTGCT	5270
QY	4506	CGCTCGATCGGATGTTTTCGGCTTGGTGTGCGAATGGGCAAGTAGCCGATCAACGCGTATGC	4565
Db	5271	CGCTCGATCGGATGTTTTCGGCTTGGTGTGCGAATGGGCAAGTAGCCGATCAACGCGTATGC	5330
QY	4566	AGCGCGCGCATTTGCATCAGCCCATGATGGATACTTTCTTCGGCAGGAGCAAGGTGAGATGAC	4625
Db	5331	AGCGCGCGCATTGATCATCAGCCCATGATGGATACTTTCTTCGGCAGGAGCAAGGTGAGATGAC	5390
QY	4626	AGGAGATCTCGCCCGGCACTTCGCCCAATPAGACGCGAGTCCCTTCGCGCTTCAGGTGACA	4685
Db	5391	AGGAGATCTCGCCCGGCACTTCGCCCAATPAGACGCGAGTCCCTTCGCGCTTCAGGTGACA	5450
QY	4686	ACGTTCGAGCACAGCTGCGCAAGGAAACGCCGCTCGTGGCCAGCACACCATAGCCGCGTGCC	4745
Db	5451	ACGTTCGAGCACAGCTGCGCAAGGAAACGCCGCTCGTGGCCAGCACACCATAGCCGCGTGCC	5510
QY	4746	TCGTCTTCGAGTTCATTTACGGGCAACCGGACAGGTTCGTCTTTGACAAAAGAACCGGCGCG	4805
Db	5511	TCGTCTTCGAGTTCATTTACGGGCAACCGGACAGGTTCGTCTTTGACAAAAGAACCGGCGCG	5570
QY	4806	CCCTGCGCTGACAGCCGGAAACA CGCGGGCATACAGACGCGGATTTGTCTTTGTGCCCAG	4865
Db	5571	CCCTGCGCTGACAGCCGGAAACA CGCGGGCATACAGACGCGGATTTGTCTTTGTGCCCAG	5630
QY	4866	TCATAGCCGAATAGCCTCTCCACCAAGCGGCGGAGAACCTCGGTGCAATCCATCTTGT	4925
Db	5631	TCATAGCCGAATAGCCTCTCCACCAAGCGGCGGAGAACCTCGGTGCAATCCATCTTGT	5690
QY	4926	TCAATCATGCGAAACGATCTCATCTCTGTCTCTTTGATTCAGATCTTGTATCCCTTCGCGCAT	4985
Db	5691	TCAATCATGCGAAACGATCTCATCTCTGTCTCTTTGATTCAGATCTTGTATCCCTTCGCGCAT	5750
QY	4986	CAG 4988	
Db	5751	CAG 5753	

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RESULT 10
US-10-811-028A-4
; Sequence 4, Application US/10811028A
; Publication No. US20050043258A1
; GENERAL INFORMATION:
; APPLICANT: Bennett, Michael
; APPLICANT: Chen, Yen-Ju
; APPLICANT: Generic, Inc.
; TITLE OF INVENTION: Methods of Treating Xerostomia and Xerophthalmia
; FILE REFERENCE: 020714-002410US
; CURRENT APPLICATION NUMBER: US/10/811,028A
; CURRENT FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: US 60/458,793
; PRIOR FILING DATE: 2003-03-26
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 5760
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:pMB1-Mt-CAT
; OTHER INFORMATION: plasmid expression vector
US-10-811-028A-4

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Query Match	32.1%	Score 1697.8;	DB 21;	Length 5760;
Best Local Similarity	86.7%;	Pred. No. 0;		
Matches 1980;	Conservative 0;	Mismatches 102;	Indels 201;	Gaps 2;
QY	2706	CTAGACGTAATCATGGTCATAGCTGTTTCTCGTGTGAAATTTGTTATCCGCTCACAAATTC		2765
DB	3679	CTTGGCGTAATCATGGTCATAGCTGTTTCTCGTGTGAAATTTGTTATCCGCTCACAAATTC		3738

QY	2766	ACACACATACGAGCCGGAAGCAATAAGTGTAAAGCTTGGGGTGCCTAATGAGTGAGCTA	2825
Db	3739	ACACACATACGAGCCGGAAGCAATAAGTGTAAAGCTTGGGGTGCCTAATGAGTGAGCTA	3798
QY	2826	ACTCACATTAATTCGGTTGGCTCAGTCCCGCTTTCCAGTCGGGAAACCTGCTGCCA	2885
Db	3799	ACTCACATTAATTCGGTTGGCTCAGTCCCGCTTTCCAGTCGGGAAACCTGCTGCCA	3858
QY	2886	GCTGCATTAATGAATCCGGCAACCGCGGGAGAGCGGTTTGGTATTCGGGGCTCTTC	2945
Db	3859	GCTGCATTAATGAATCCGGCAACCGCGGGAGAGCGGTTTGGTATTCGGGGCTCTTC	3918
QY	2946	CGCTTCCTCGCTCACTGACTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCT	3005
Db	3919	CGCTTCCTCGCTCACTGACTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCT	3978
QY	3006	TCACCTCAAGGCGGTATACGGTTATCCACAGAAATCAGGGGATTAACCGAGAAAGACAT	3065
Db	3979	TCACCTCAAGGCGGTATACGGTTATCCACAGAAATCAGGGGATTAACCGAGAAAGACAT	4038
QY	3066	GTGAGCAAAAGGCCAGCAAAAGGCCAGCAACCGTAAAGGCCGCTGCTGGCGTTTTT	3125
Db	4039	GTGAGCAAAAGGCCAGCAAAAGGCCAGCAACCGTAAAGGCCGCTGCTGGCGTTTTT	4098
QY	3126	CCATAGGCTCCGCCCTCTGACGAGCATCAAAAAATCGACGCTCAAGTCAGAGGTGGCG	3185
Db	4099	CCATAGGCTCCGCCCTCTGACGAGCATCAAAAAATCGACGCTCAAGTCAGAGGTGGCG	4158
QY	3186	AAACCCGACAGGACTATAAAGATACACAGGCGTTTCCCTCGGAAGTCCCTCGTGGCTC	3245
Db	4159	AAACCCGACAGGACTATAAAGATACACAGGCGTTTCCCTCGGAAGTCCCTCGTGGCTC	4218
QY	3246	TCCTGTTCCGACCTCGCGTTACCGGATACCTGTCGCGCTTCTCCCTTCGGGAGCGT	3305
Db	4219	TCCTGTTCCGACCTCGCGTTACCGGATACCTGTCGCGCTTCTCCCTTCGGGAGCGT	4278
QY	3306	GGCGCTTTCTCATAGCTCAGCTGTAGGTATCTCAGTTCCGTTAGGTGCTCGTCCAA	3365
Db	4279	GGCGCTTTCTCATAGCTCAGCTGTAGGTATCTCAGTTCCGTTAGGTGCTCGTCCAA	4338
QY	3366	GCTGGGCTGTGACAGAAACCCCGCTTACGCGGACCGCTGCGCTTATCCGGTAACTA	3425
Db	4339	GCTGGGCTGTGACAGAAACCCCGCTTACGCGGACCGCTGCGCTTATCCGGTAACTA	4398
QY	3426	TCGCTTTGAGTCCAAACCGGTAGACACGACTTATCCGCACTGGCAGCAGCCACTGGTAA	3485
Db	4399	TCGCTTTGAGTCCAAACCGGTAGACACGACTTATCCGCACTGGCAGCAGCCACTGGTAA	4458
QY	3486	CAGGATTTAGCAGAGCGAGGTATGTAGCGGTGCTTACAGAGTCTTGAAGTGGTGGCTAA	3545
Db	4459	CAGGATTTAGCAGAGCGAGGTATGTAGCGGTGCTTACAGAGTCTTGAAGTGGTGGCTAA	4518
QY	3546	CTACGGCTACACTAGAGAAACAGATTTGGTATCTCGCTCTGCTGAAGCCAGTTACCTT	3605
Db	4519	CTACGGCTACACTAGAGAAACAGATTTGGTATCTCGCTCTGCTGAAGCCAGTTACCTT	4578
QY	3606	CGGAAAGAGTTGGTAGCTCTTGATCCGCAACAAACACCGCTGCTGGTAGCGGTGTTT	3665
Db	4579	CGGAAAGAGTTGGTAGCTCTTGATCCGCAACAAACACCGCTGCTGGTAGCGGTGTTT	4638
QY	3666	TTTTTTTTCAGCAGCAGATTAACGCGCAAAAAAGGATCTCAAGAGATCCTTTGAT	3725
Db	4639	TTTTTTTTCAGCAGCAGATTAACGCGCAAAAAAGGATCTCAAGAGATCCTTTGAT	4698
QY	3726	CTTTTCTACGGGGTCTGACGCTCAGTGGAAACGAAACTCACTGAAGGATTTTGGTCAAT	3785
Db	4699	CTTTTCTACGGGGTCTGACGCTCAGTGGAAACGAAACTCACTGAAGGATTTTGGTCAAT	4758
QY	3786	GAGATTTATCGTACCAAGCGGCATCGTGGCTTCCCACTCTCTGCAAGTTTCGGGGCATG	3845
Db	4759	GAG-----	4761
QY	3846	GATCGCGGATAGCCGCTGCTGCTTCTCGATCCGACGGAATTCGACTGCCGTTAGAA	3905
Db	4762	-----	4761
QY	3906	CTCCGCGAGGTCTCGAGCCTCAGGCGAGCAGCTGAACCAACTCCGAGGGGATCGAGCCC	3965
Db	4762	-----CGGATACATATTTGAAATGATTTAGAAAAATAAACAATAAG	4802
QY	3966	GGGGTGGCGGAAGAACTCCAGCATGAGTCCCGCTCGAGGATCATCCAGCCGGGCTC	4025
Db	4803	GGGGTGGCGGAAGAACTCCCGGAAAGTGCCACTGTATGCGGTGTGAATATCCGCAAG	4862
QY	4026	CCGAAAAACGATTTCCGAAGCCAACTTTTCATAGAGGCGCGGTGGAATCGAAATCTCG	4085
Db	4863	ATCGTTAAGGAGAAAAATACCGCATCAGGAAATTTGAAGCGTTAATAAT	4910
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Db	4911	-----TCAGAG	4917
QY	4146	AACCTCGTCAAGAGGCGATAGAGGCGATGCGCTCGGATTCGGAGCGGCGATACCGTAA	4205
Db	4918	AACCTCGTCAAGAGGCGATAGAGGCGATGCGCTCGGATTCGGAGCGGCGATACCGTAA	4977
QY	4206	AGCACGAGGAAGCGGTACGCCCATTCGCGCCCAAGCTCTTTACGCAATATCACGGGTAGCC	4265
Db	4978	AGCACGAGGAAGCGGTACGCCCATTCGCGCCCAAGCTCTTTACGCAATATCACGGGTAGCC	5037
QY	4266	AAGCTATGTCTGTATAGGCTCCGCCACACCCAGCGGCGCACAGTCGATGAATTCAGAA	4325
Db	5038	AAGCTATGTCTGTATAGGCTCCGCCACACCCAGCGGCGCACAGTCGATGAATTCAGAA	5097
QY	4326	AAGCGGCCATTTTCCACCATGATATTTCGCAAGCAGGCGATCCGATGGGTACAGACAGA	4385
Db	5098	AAGCGGCCATTTTCCACCATGATATTTCGCAAGCAGGCGATCCGATGGGTACAGACAGA	5157
QY	4386	TCCTCCCGCTCGGGCATCGCGCTTGAAGCTTGGCGAAACAGTTTCGGCTGGCGGAGCCCC	4445
Db	5158	TCCTCCCGCTCGGGCATCGCGCTTGAAGCTTGGCGAAACAGTTTCGGCTGGCGGAGCCCC	5217
QY	4446	TGATGCTCTTGTCTCAGATCATCTGATCGAAGAACCCGGCTTCCATCCGAGTACGTGCT	4505
Db	5218	TGATGCTCTTGTCTCAGATCATCTGATCGAAGAACCCGGCTTCCATCCGAGTACGTGCT	5277
QY	4506	CGCTCGATCGGATGTTTCGCTTGGTGGTTCGATTCGCGAGTACCGGATCAAGCGTATGC	4565
Db	5278	CGCTCGATCGGATGTTTCGCTTGGTGGTTCGATTCGCGAGTACCGGATCAAGCGTATGC	5337
QY	4566	AGCCGCGCATTTGCAATCAGCCATGATGATATCTTCTCGGAGGAGCAAGGTGAGATGAC	4625
Db	5338	AGCCGCGCATTTGCAATCAGCCATGATGATATCTTCTCGGAGGAGCAAGGTGAGATGAC	5397
QY	4626	AGGAGATCTGCTCCCGGCACTTTCGCGCAATAGCAGCAGTCCCTTCCCGCTTCAGTGACA	4685
Db	5398	AGGAGATCTGCTCCCGGCACTTTCGCGCAATAGCAGCAGTCCCTTCCCGCTTCAGTGACA	5457
QY	4686	AGGTTCGAGCACAGCTTCGCAAGAACCGCGCTGCTGGCCAGCCACGATAGCGCGTGC	4745
Db	5458	AGGTTCGAGCACAGCTTCGCAAGAACCGCGCTGCTGGCCAGCCACGATAGCGCGTGC	5517
QY	4746	TGCTCTCGCAGTTTTCATTTCAGGCGCACCGGACAGTTCGCTTTCGCAAAAAAGAACCGGGCGC	4805
Db	5518	TGCTCTCGCAGTTTTCATTTCAGGCGCACCGGACAGTTCGCTTTCGCAAAAAAGAACCGGGCGC	5577
QY	4806	CCCTGCGCTGACAGCGGGAACACCGCGGATCAGAGCAGCCGATTTGTTGTGCCAG	4865
Db	5578	CCCTGCGCTGACAGCGGGAACACCGCGGATCAGAGCAGCCGATTTGTTGTGCCAG	5637
QY	4866	TATAGCCGAATAGCTCTTCCACCCAGCGGCGGAGAACCTCGCTGCAATTCATTTGT	4925
Db	5638	TATAGCCGAATAGCTCTTCCACCCAGCGGCGGAGAACCTCGCTGCAATTCATTTGT	5697
QY	4926	TCAATCATCGGAACGATCTCTCTCTTGTATCAGATCTTGTATCCCTCGGCCAT	4985


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QY 4391 GCGCTGGGCGATGCGCGCTTGAGCTGGCGGAAAGTTCGGCTGGCGGAGCCCTGATG 4450
Db 3545 GCGCTGGGCGATGCTCGCTTGAGCTGGCGGAAAGTTCGGCTGGCGGAGCCCTGATG 3486
QY 4451 CTCCTTCGTCAGATCATCTGATCGACAAAGACCGGTTCCATCCGAGTACGTGCTGCTC 4510
Db 3485 CTCCTTCGTCAGATCATCTGATCGACAAAGACCGGTTCCATCCGAGTACGTGCTGCTC 3426
QY 4511 GATCGGATGTTTCGCTTGGTGGTCCGAATGGCGAGGTAGCCGGATCAAGCGTATGACGCCG 4570
Db 3425 GATCGGATGTTTCGCTTGGTGGTCCGAATGGCGAGGTAGCCGGATCAAGCGTATGACGCCG 3366
QY 4571 CCGCATTTGCATCAGCATGATGATGATCTTCTTCGGCAGGACAAAGTGCAGAGGAG 4630
Db 3365 CCGCATTTGCATCAGCATGATGATGATCTTCTTCGGCAGGACAAAGTGCAGAGGAG 3306
QY 4631 ATCTGCGCCCGGCACTTCGCCCAATAGCAGCAGTCCCTTCGCGCTTCAGTGACAAAGTC 4690
Db 3305 ATCTGCGCCCGGCACTTCGCCCAATAGCAGCAGTCCCTTCGCGCTTCAGTGACAAAGTC 3246
QY 4691 GAGCACAGCTGCGCAAGGAAAGCGCCGTCGTGGCCAGCCAGATAGCCGCTGCTGCTC 4750
Db 3245 GAGCACAGCTGCGCAAGGAAAGCGCCGTCGTGGCCAGCCAGATAGCCGCTGCTGCTC 3186
QY 4751 CTGAGTTCAITTCAGGGGACCGGACAGTTCGTCTTGACAAAAGAACCCGGCGCCCTG 4810
Db 3185 TTGAGTTCAITTCAGGGGACCGGACAGTTCGTCTTGACAAAAGAACCCGGCGCCCTG 3126
QY 4811 CGCTGACAGCGGGAACAGCGGCATCAGAGCAGCGGATGCTGTTGTGCGCCAGTCATA 4870
Db 3125 CGCTGACAGCGGGAACAGCGGCATCAGAGCAGCGGATGCTGTTGTGCGCCAGTCATA 3066
QY 4871 GCGCAATAGCTCTTCCACCAAGCGCGGAGAACCTGCGTGCAATCCATCTTGTTCAT 4930
Db 3065 GCGCAATAGCTCTTCCACCAAGCGCGGAGAACCTGCGTGCAATCCATCTTGTTCAT 3006
QY 4931 CATGCGAAAGATCTCATCTGCTTCATGATCAGATCTTGTGATCCCTGCGGCATCAGAT 4990
Db 3005 CATGCGAAAGATCTCATCTGCTTCATGATCAGATCTTGTGATCCCTGCGGCATCAGAT 2946
QY 4991 CCTTGGCGGCAAGAAAGCAATCCAGTTTACCTTTCAGGGGCTTCCCACTTACAGAGG 5050
Db 2945 CCTTGGCGGCAAGAAAGCAATCCAGTTTACCTTTCAGGGGCTTCCCACTTACAGAGG 2886
QY 5051 CGCCCGAGCTGGCAATTCGGGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5110
Db 2885 CGCCCGAGCTGGCAATTCGGGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2826
QY 5111 CCATGTAAGCCCACTGCAAGTACCTGCTTCTTTCGCTGCTGCTGCTGCTGCTGCTGCT 5170
Db 2825 CCATGTAAGCCCACTGCAAGTACCTGCTTCTTTCGCTGCTGCTGCTGCTGCTGCTGCT 2766
QY 5171 GATAGCCAGTGTGATTCATTCGGGCTGAGCAGCGTTCTGCGGACTGCGCTTCTTCTA 5230
Db 2765 GATAGCCAGTGTGATTCATTCGGGCTGAGCAGCGTTCTGCGGACTGCGCTTCTTCTA 2706
QY 5231 CGTG 5234
Db 2705 CGTG 2702
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RESULT 12

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US-10-790-455-10/c
; Sequence 10, Application US/10790455
; Publication No. US20040210954A1
; GENERAL INFORMATION:
; APPLICANT: Avigenics, Inc
; TITLE OF INVENTION: Avian Integrase-mediated Transformation
; FILE REFERENCE: A181 1080.1
; CURRENT APPLICATION NUMBER: US/10790,455
; FILING DATE: 2004-03-01
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.2
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; SEQ ID NO 10
; LENGTH: 6233
; TYPE: DNA
; ORGANISM: Plasmid pCR-XL-TOPO-CMV-pur-attB
US-10-790-455-10
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Query Match 30.9%; Score 1634.4; DB 20; Length 6233;
Best Local Similarity 80.6%; Pred. No. 0;
Matches 2082; Conservative 0; Mismatches 211; Indels 291; Gaps 3;

QY 2942 CTTTCGCTTCCTCGCTCACTGACTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCT 3001
Db 6233 CTTTCGCTTCCTCGCTCACTGACTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCT 6174
QY 3002 CAGCTCACTCAAAAGGCGGTAATACAGGTATTCACAGAAATCAGGGGATTAACGAGGAAAGA 3061
Db 6173 CAGCTCACTCAAAAGGCGGTAATACAGGTATTCACAGAAATCAGGGGATTAACGAGGAAAGA 6114
QY 3062 ACATGTAGCAAAAGGCGGCAAGGCAAGGCAAGGCAAGGCAAGGCAAGGCAAGGCAAGGCA 3121
Db 6113 ACATGTAGCAAAAGGCGGCAAGGCAAGGCAAGGCAAGGCAAGGCAAGGCAAGGCAAGGCA 6054
QY 3122 TTTTTCATAGGCTCCGCGCCCTCGAGAGGATCAGAAATCAGCGCTCAAGTCAGAGGT 3181
Db 6053 TTTTTCATAGGCTCCGCGCCCTCGAGAGGATCAGAAATCAGCGCTCAAGTCAGAGGT 5994
QY 3182 GCGGAAACCGCAGCAGGACTATTAAGATACAGGCGCTTCCCGCTGGAAGCTCCCTCGTGC 3241
Db 5993 GCGGAAACCGCAGCAGGACTATTAAGATACAGGCGCTTCCCGCTGGAAGCTCCCTCGTGC 5934
QY 3242 GCTCTCTCTGTTCCGACCTTCGCGCTTACCGGATACCTGTCGCGCTTCTCTCTTCGCGAA 3301
Db 5933 GCTCTCTCTGTTCCGACCTTCGCGCTTACCGGATACCTGTCGCGCTTCTCTCTTCGCGAA 5874
QY 3302 GCGTGGCGCTTCTCATAGCTCACTGCTGAGTATCTCAGTTCGGTGTAGTTCGCTCGCT 3361
Db 5873 GCGTGGCGCTTCTCATAGCTCACTGCTGAGTATCTCAGTTCGGTGTAGTTCGCTCGCT 5814
QY 3362 CAAAGCTGGGCTGTGTGACGAAACCCCGCTTACGAGCCGACCGCTCGCTTCATCCGGTA 3421
Db 5813 CAAAGCTGGGCTGTGTGACGAAACCCCGCTTACGAGCCGACCGCTCGCTTCATCCGGTA 5754
QY 3422 ACTATCGTCTTGAGTCCAAACCCGGTAAAGACAGACTTATCGCCACTGGCAGCAGCACCTG 3481
Db 5753 ACTATCGTCTTGAGTCCAAACCCGGTAAAGACAGACTTATCGCCACTGGCAGCAGCACCTG 5694
QY 3482 GTAAAGAGATTAGCAGAGAGGATGTAGGGCGTCTACAGAGTCTTGAAGTGTGTGC 3541
Db 5693 GTAAAGAGATTAGCAGAGAGGATGTAGGGCGTCTACAGAGTCTTGAAGTGTGTGC 5634
QY 3542 CTAACCTACCGCTACACTAGAAGACAGTATTTGGTATCTGCGCTCTGCTGAGCCAGTTA 3601
Db 5633 CTAACCTACCGCTACACTAGAAGACAGTATTTGGTATCTGCGCTCTGCTGAGCCAGTTA 5574
QY 3602 CCTTCGGAAGAGAGTGTGTAGTCTTGTATCCGGCAAAACAAACCCAGCTGTGTAGCGGTG 3661
Db 5573 CCTTCGGAAGAGAGTGTGTAGTCTTGTATCCGGCAAAACAAACCCAGCTGTGTAGCGGTG 5514
QY 3662 GTTTTTTTTGTGAAGCAGAGATTAACCGCAGAGAAAAAGGATCTCAAGAGATCTT 3721
Db 5513 GTTTTTTTTGTGAAGCAGAGATTAACCGCAGAGAAAAAGGATCTCAAGAGATCTT 5454
QY 3722 TGATCTTTTCTACGGGCTGCTGAGCTCAGTGGAACGAAATCAGCTGAGGATTTTGG 3781
Db 5453 TGATCTTTTCTACGGGCTGCTGAGCTCAGTGGAACGAAATCAGCTGAGGATTTTGG 5394
QY 3782 TCATGAGATTATC----- 3794
Db 5393 TCATGAGATTATCAAAAGGATCTTCCACTAGATCTTTAAATTAATAATGAGTTT 5334
QY 3795 ----- 3802
Db 5333 GCACGTGTCACTGCTCTCTCGGCCAGGAGTGACGAGTTGCGGCGCGGTGCGCA 5274
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QY 3803 AAGCGGCATCGTGCCTCCCACTCTCGAGTTCCGGGCGATGATGCGGGATAGCCGC 3862
Db |||||
QY 5273 GGGCGAACTCCCGCCCCAGCGTGTCTGCGCGATCTCGGTTCATGGCCGGCCGGAGCGCT 5214
Db |||||
QY 3863 TGTGTGTTTCTTGATGCGGACCGGATTTGCACTGCGGCTAGAACTCCGGGAGTCTGTCCA 3922
Db |||||
QY 5213 CCGGAAGTTCTGGGACACGACCTCCGACCTCGGCGTACAGCTCGTCCAGCCCGGCA 5154
QY 3923 GCC----- 3925
Db ||
QY 5153 CCACACCCAGGCCAGGCTGTGTCCGGCACCACTGGTCTCTGGAACCGGCTGATGAACA 5094
QY 3926 ---TCAGGCAGAGCTGAACCAACTCGGAGGGGATCGAGCCGGGTTGGCGAAGAACT 3982
Db |||||
QY 5093 GGGTCACGTGTCCTCCGGACACACCGCGGAAGTCGTCTCCACGAAATCCCGGGAGAAC 5034
QY 3983 CCAGCATGAGATCCCGCGCTGAGGATCATCCAGCGCGCTCCCGAAAAACGATTCCGA 4042
Db |||||
QY 5033 CGAGCCGTTCGATCAGAACTCGACCGCTCCGGCGAGCTCGCGCGGTGAGCACCGGAA 4974
QY 4043 AGCCCAACCTTTCATAGAGCGCGGTGGAATCGAAATCTCGTGATGGCAGGTTGGCG 4102
Db |||||
QY 4973 CGGCACTGGTCAACTTGGGCATGGTGGCCCTCTCACGTGCTATTATTGAAGCATTTATC 4914
QY 4103 TCGCTTGGTCCGTCACTTCGAACCCAGAGTCCCG----- 4137
Db |||||
QY 4913 AGGGTTATTGTCATGAGCGGATACATATTTGAATGTATTAGAAAAATAACAATAG 4854
QY 4138 ----- 4137
Db |||||
QY 4853 GGGTTCGGGCACATTTCCCGGAAAGTCCCACTGTATGCGGTGTGAATACCGCACAG 4794
QY 4138 -----CTCAGAAGAACTC 4150
Db |||||
QY 4793 ATCGTTAAGGAGAAAAATACCGCATCAGGAAATGTAAGCGTTAATAATTGAGAAGAACTC 4734
QY 4151 GTCAGAGCGGATAGAGCGATGCGTTCGATCGGAGCGGCGGATACCGTAAAGCAC 4210
Db |||||
QY 4733 GTCAAGAGCGGATAGAGCGGATGCGTTCGATCGGAGCGGCGGATACCGTAAAGCAC 4674
QY 4211 GAGGAAGCGGTACAGCCATTCGCGCCCAAGCTCTTCAGCAATATCACGGGTAGCCAAACG 4270
Db |||||
QY 4673 GAGGAAGCGGTACAGCCATTCGCGCCCAAGCTCTTCAGCAATATCACGGGTAGCCAAACG 4614
QY 4271 TATGTCTGTATAGCGGTTCGCGCACACCCAGCGGCGCACAGTCGATGAATCCAGAAAGCG 4330
Db |||||
QY 4613 TATGTCTGTATAGCGGTTCGCGCACACCCAGCGGCGCACAGTCGATGAATCCAGAAAGCG 4554
QY 4331 GCCATTTTCCACCATGATATTCGGCAAGCAGGATCGCCATGGGTCAACGAGATCCTC 4390
Db |||||
QY 4553 GCCATTTTCCACCATGATATTCGGCAAGCAGGATCGCCATGGGTCAACGAGATCCTC 4494
QY 4391 GCCGTTCGGGCATCGCGCCCTTGAGCTTCGCGAAACAGTTGCGGTGGCGCGAGCCCTGATG 4450
Db |||||
QY 4493 GCCGTTCGGGCATCGCTCGCTTGAGCTTCGCGAAACAGTTGCGGTGGCGCGAGCCCTGATG 4434
QY 4451 CTCTTCGTTCAGATCATCTGTATCGCAAGACCGGTTTCATCCGAGTACGTCTCGCTC 4510
Db |||||
QY 4433 CTCTTCGTTCAGATCATCTGTATCGCAAGACCGGTTTCATCCGAGTACGTCTCGCTC 4374
QY 4511 GATCGCATGTTTCGCTTGGTGGTTCGAATGGGCAAGGTAGCCGATCAAGCTATGAGCCG 4570
Db |||||
QY 4373 GATGCGATGTTTCGCTTGGTGGTTCGAATGGGCAAGGTAGCCGATCAAGCTATGAGCCG 4314
QY 4571 CCCCATTTGATCAGCATGATGATATCTTCTCGGAGAGCAAGGTGAGATCAGAGGAG 4630
Db |||||
QY 4313 CCGCATTTGATCAGCATGATGATATCTTCTCGGAGAGCAAGGTGAGATGAGAGGAG 4254
QY 4631 ATCTGCGCCCGGCACTTTCGCGCCCAATAGAGCCAGTCCCTTTCGCTTTCAGTGAACGTC 4690
Db |||||
QY 4253 ATCTGCGCCCGGCACTTTCGCGCCCAATAGAGCCAGTCCCTTTCGCTTTCAGTGAACGTC 4194
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Db |||||
QY 4193 GAGCACAGTTCGCAAGGAAACCGCGTCTGTGCGCAGCCACGATAGCCGCGTGCCTCGTC 4134
QY 4751 CTGCAAGTTTCATTTCAGGACACCGGACAGGTCGCTTGTGACAAAGAACCGGCGCCCTG 4810
Db |||||
QY 4133 TTGCAAGTTTCATTTCAGGACACCGGACAGGTCGCTTGTGACAAAGAACCGGCGCCCTG 4074
QY 4811 CGCTGACAGCCGGAACACCGCGGCGATCAGAGCAGCGGATGTGTGTGCGCCAGTCATA 4870
Db |||||
QY 4073 CGCTGACAGCCGGAACACCGCGGCGATCAGAGCAGCGGATGTGTGTGCGCCAGTCATA 4014
QY 4871 GCGCAATAGCTCTCCACCCAGCGCGAGAACTGCGTCAATTCATCTTTGTTCAAT 4930
Db |||||
QY 4013 GCGCAATAGCTCTCTCACCAAGCGCGGAGAACTGCGTCAATTCATCTTTGTTCAAT 3954
QY 4931 CATGGAACAGATCTCTCTCTCTTGTGATCAGATCTTGTATCCCTGCGCCATCAGAT 4990
Db |||||
QY 3953 CATGGAACAGATCTCTCTCTCTTGTGATCAGAGCTTGTATCCCTGCGCCATCAGAT 3894
QY 4991 CTTTGGCGGCAAGAAAGCCATCCAGTTTACCTTTCAGGCGTTCCTCAACCTTACCAGAGG 5050
Db |||||
QY 3893 CTTTGGCGGCAAGAAAGCCATCCAGTTTACCTTTCAGGCGTTCCTCAACCTTACCAGAGG 3834
QY 5051 CGCCCCAGCTGGCAATTCGCGTTCGCTCTGCTCCATAAACCGCCAGTCTAGCTATCG 5110
Db |||||
QY 3833 CGCCCCAGCTGGCAATTCGCGTTCGCTCTGCTCCATAAACCGCCAGTCTAGCTATCG 3774
QY 5111 CCATGTAAGCCCACTGCAAGCTTACCTGCTTCTCTTTCGCGTTCGCTTTTCCCTTGTCCA 5170
Db |||||
QY 3773 CCATGTAAGCCCACTGCAAGCTTACCTGCTTCTCTTTCGCGTTCGCTTTTCCCTTGTCCA 3714
QY 5171 GATAGCCAGTACGATGACATTCATTCGCGGTCAGACCGTTCCTGCGGACTGCTTTCTA 5230
Db |||||
QY 3713 GATAGCCAGTACGATGACATTCATTCGCGGTCAGCACCGTTCCTGCGGACTGCTTTCTA 3654
QY 5231 CGTG 5234
Db 3653 CGTG 3650
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RESULT 13

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US-10-811-136B-10/c
; Sequence 10, Application US/10811136B
; Publication No. US20040255345A1
; GENERAL INFORMATION:
; APPLICANT: AviGenics, Inc
; TITLE OF INVENTION: Production of a Transgenic Avian by Cytoplasmic Injection
; FILE REFERENCE: AVI-025CIPCT
; CURRENT APPLICATION NUMBER: US/10/811,136B
; CURRENT FILING DATE: 2004-03-26
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
; LENGTH: 6233
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Plasmid pCR-XL-TOPO-CMV-pur-attB
US-10-811-136B-10
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Query Match 30.9%; Score 1634.4; DB 20; Length 6233;
Best Local Similarity 80.6%; Pred. No. 0;
Matches 2082; Conservative 0; Mismatches 211; Indels 291; Gaps 3;

QY 2942 CTTCCGCTTCCTCGCTCACTGACTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTAT 3001
Db |||||
QY 6233 CTTCCGCTTCCTCGCTCACTGACTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTAT 6174
Db |||||
QY 3002 CAGCTCACTCAAAAGCGGTAATACGGTTATCCACAGATCAGGGGATTAACGAGGAAAGA 3061
Db |||||
QY 6173 CAGCTCACTCAAAAGCGGTAATACGGTTATCCACAGATCAGGGGATTAACGAGGAAAGA 6114
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Db 3953 CATGCGAAACGATCCTCATCTGCTCTTGATCAGAGCTTGATCCCTCGCGCATCAGAT 3894
QY 4991 CCTTGGCGGCAAGAAAGCCATCCAGTTTACTTTGCGAGGGCTTCCCAACCTTACCAGAGG 5050
Db 3893 CCTTGGCGGCGAAGAAAGCCATCCAGTTTACTTTGCGAGGGCTTCCCAACCTTACCAGAGG 3834
QY 5051 CGCCCCAGCTGGCAATTCGGGTTCCGTTGCTGTCGTCGATATAAAACCGCCAGCTAGCTATCG 5110
Db 3833 CGCCCCAGCTGGCAATTCGGGTTCCGTTGCTGTCGTCGATATAAAACCGCCAGCTAGCTATCG 3774
QY 5111 CCATGTAAGCCCACTGCAAGCTACCTGCTTCTCTTTGGGCTTGGCTTTTCCCTTGTCCA 5170
Db 3773 CCATGTAAGCCCACTGCAAGCTACCTGCTTCTCTTTGGGCTTGGCTTTTCCCTTGTCCA 3714
QY 5171 GATAGCCAGTAGCTGACATTCATCCGGGTCAGACCGGTTCTGCGGACTGGCTTTCTA 5230
Db 3713 GATAGCCAGTAGCTGACATTCATCCGGGTCAGACCGGTTCTGCGGACTGGCTTTCTA 3654
QY 5231 CGTG 5234
Db 3653 CGTG 3650

RESULT 14

US-10-940-315-10/c
; Sequence 10, Application US/10940315
; Publication No. US20050034186A1
; GENERAL INFORMATION:
; APPLICANT: Avigenics, Inc
; TITLE OF INVENTION: Site Specific Nucleic Acid Integration
; FILE REFERENCE: AVI-025CIP3
; CURRENT APPLICATION NUMBER: US/10/940,315
; CURRENT FILING DATE: 2004-09-14
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
; LENGTH: 6233
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Plasmid pCR-XL-TOPO-CMV-pur-attB
US-10-940-315-10

Query Match 30.9%; Score 1634.4; DB 21; Length 6233;

Best Local Similarity 80.6%; Pred. No. 0;

Matches 2082; Conservative 0; Mismatches 211; Indels 291; Gaps 3;

QY 2942 CTTCCGCTTCTCGCTCACTGACTCGCTGGCTCGGTTCGTTGGCTCGCGCAGCGGTAT 3001
Db 6233 CTTCCGCTTCTCGCTCACTGACTCGCTGGCTCGGTTCGTTGGCTCGCGCAGCGGTAT 6174
QY 3002 CAGCTCACTCAAAAGCGGTAATACGGTTATCCACAGAAATCAGGGGATAACGCAAGAAAGA 3061
Db 6173 CAGCTCACTCAAAAGCGGTAATACGGTTATCCACAGAAATCAGGGGATAACGCAAGAAAGA 6114
QY 3062 ACATGTAGCAAAAGCGCAGCAAAAGCCAGGAAACGTTAAAGAGCGCGGTCTCGCGGT 3121
Db 6113 ACATGTAGCAAAAGCGCAGCAAAAGCCAGGAAACGTTAAAGAGCGCGGTCTCGCGGT 6054
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Db 6053 TTTTTCATAGGCTCCGCCCTCGAGCATCACAAAATCGACGCTCAAGTCAGAGGT 5994
QY 3182 GCGCAACCCGACAGGACTATAAGATACACAGCGTTTCCCTCGGAAGCTCCCTCGTGC 3241
Db 5993 GCGCAACCCGACAGGACTATAAGATACACAGCGTTTCCCTCGGAAGCTCCCTCGTGC 5934
QY 3242 GCTCTCTGTTCCGACCCCTGCGGTTACCGGATACCTGTCGCGCTTCTCCCTTCGGAA 3301
Db 5933 GCTCTCTGTTCCGACCCCTGCGGTTACCGGATACCTGTCGCGCTTCTCCCTTCGGAA 5874
QY 3302 CGGTGGCGCTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCTCGTTCGCT 3361

Db 5873 GCGTGGCGCTTTCTCATAGCTCACGCTGATAGGTATCTCAGTTCGGTGTAGGTCTCGCT 5814
QY 3362 CCAAGCTGGGCTGTGTGCAAGAAACCCCGGTTACGCCGACCGCTGCGCTTATCCGGTA 3421
Db 5813 CCAAGCTGGGCTGTGTGCAAGAAACCCCGGTTACGCCGACCGCTGCGCTTATCCGGTA 5754
QY 3422 ACTATCGTCTTCAAGTCCAAACCCGTTAAGACACAGCTTATCGCCACTTGGCAGCAGCACATG 3481
Db 5753 ACTATCGTCTTCAAGTCCAAACCCGTTAAGACACAGCTTATCGCCACTTGGCAGCAGCACATG 5694
QY 3482 GTAAACAGGATTACGAGCGAGGTATGTAGGGGGTGTCTACAGAGTTCTTTGAAGTGGTGC 3541
Db 5693 GTAAACAGGATTACGAGCGAGGTATGTAGGGGGTGTCTACAGAGTTCTTTGAAGTGGTGC 5634
QY 3542 CTAACTACGGCTACACTAGAAACACAGTTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTA 3601
Db 5633 CTAACTACGGCTACACTAGAAACACAGTTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTA 5574
QY 3602 CCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAACAAACACCGCTGTAGCGGTG 3661
Db 5573 CCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAACAAACACCGCTGTAGCGGTG 5514
QY 3662 GTTTTTTTTGTTCGAAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAGATCCTT 3721
Db 5513 GTTTTTTTTGTTCGAAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAGATCCTT 5454
QY 3722 TGATCTTTTCTACGGGCTCTGACGCTCAGTGGAACGAAACCTCACGTTAAGGATTTTGG 3781
Db 5453 TGATCTTTTCTACGGGCTCTGACGCTCAGTGGAACGAAACCTCACGTTAAGGATTTTGG 5394
QY 3782 TCATGAGATTATC----- 3794
Db 5393 TCATGAGATTATCAAAAAGGATCTTCACTAGATCCTTTTAAATTAATAATGAAGTTTA 5334
QY 3795 ----- 3802
Db 5333 GCACGTGTCAAGTCTGCTCTCGGCCACGAAAGTCAGCAGATTGCCGCGGTTCGGCA 5274
QY 3803 AAGCGGCATCTGTCCTCCCACTCTCTGCAAGTTTCGGGGCATGGATCGCGGATAGCCGC 3862
Db 5273 GGGCGAACTCCCGCCGCCACGCTGCTCGCCGATCTCGGTCATGGCGCGCCCGAGGCGT 5214
QY 3863 TGCTGTTTCTTGGATGCGCGGATTTGCACTGCGCGTAGAACTCCCGAGGTCTGTCCA 3922
Db 5213 CCGGGAAGTTCTGTGACACGACTCGACCACTCGGCGTACAGCTCGTCAGGCCCGCA 5154
QY 3923 GGC----- 3925
Db 5153 CCCACACCCAGCGCGGTTGTTCGGCACCACTGCTCTGGACCGGCTGATGAACA 5094
QY 3926 ----TCAGGCAGAGCTGAACCACTCGCGAGGGGATCGAGCCCGGGGTGGCGAGAACT 3982
Db 5093 GGGTCACGTCGTCCCGGACCAACACCGCGAAGTCGCTCTCCACGAAGTCCCGGGAACC 5034
QY 3983 CCAGCATGAGATCCCGCGCTGAGGATCATCCAGCGCGCTCCCGGAAAAAGATTCCGA 4042
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QY 4043 AGCCCCACCTTTTCATAGAAAGGGGGTGGAAATCGAAATCTCGTGTAGGAGGTTCGGCG 4102
Db 4973 CGGCATCTGCTCAACTTGGCCATGGTGGCCCTCTCAGCTGCTATTATTGAAGCATTTATC 4914
QY 4103 TCGTTGGTTCGGTCAATTCGAACCCCGAGTCCCG----- 4137
Db 4913 AGGGTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAAATAAG 4854
QY 4138 ----- 4137
Db 4853 GGGTCCGCGCACATTTTCCCGAAAGTCCACCTGTATGCGGTGTGAATATCCGCACAG 4794
QY 4138 ----- 4150
Db 4793 ATGCGTAAGAGAAAAATACCGCATCAGGAAATTTGAAGCGTTAATAATTTAGAAAGATC 4734

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Db 5513 GTTTTTTTGTTGCAAGCAGCAGATTACGCGCAGAAAAAAGATCTCAAGAAGATCCTT 5454
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Db 5453 TGATCTTTTCTAGCGGGTCTGAGCTCAGTGGAGCAAACTCACGTTAAGGATTTTGG 5394
Qy 3782 TCATGAGATTATC----- 3794
Db 5393 TCATGAGATTATCAAAAAAGATCTTCACTAGATCCTTTTAAATTAATAATGAATTTTA 5334
Qy 3795 -----GTGACCA 3802
Db 5333 GCACGTGTCACTCTCTCGGCCACGAAGTGACGAGTTGCGCGCGGTGCGCA 5274
Qy 3803 AAGCGCCATCGTGCTCTCCCACTCTCGAGTTGCGGGGCATGGATGCGGGATAGCCGC 3862
Db 5273 GGGCGAACTCCCGCCCCCAAGCTGCTCGCCGATCTCGGTCAATGCGCCGCCGAGGCGT 5214
Qy 3863 TGTGCTTTTCTTGATGCGCAGCAGATTGCACTGCGGTAGAACTCCGCGAGTCTGCA 3922
Db 5213 CCGGAAGTTCTGGGACACGACTCCGACCACTCGCGGTACAGCTGTCAGGCCGCA 5154
Qy 3923 GCC----- 3925
Db 5153 CCACACCCAGGCCAGGGTGTGTCGGGCACCACTGGTCTTGGACCGGCTGATGAACA 5094
Qy 3926 ----TCAGGACAGCTGAACCACTCGCGAGGGATCGAGCCCGGGTGGCGAAGACT 3982
Db 5093 GGTGTCAGTCTCCCGACACACCGCGCAAGTCGCTCCACGAAGTCCCGGAGAAC 5034
Qy 3983 CCAGCATGATCCCCCGCTGGAGGATCATCAGCGCGGCTCCCGAAAAAGATTCCGA 4042
Db 5033 CGAGCCGGTGGTTCAGAACTCGACCGCTCCGCGAGCTGCGCGGGTGAGCACCGGA 4974
Qy 4043 AGCCCAACCTTTCATAGAGGCGGCGGTGGAAATCTCGTGATGGCAGGTTGGCG 4102
Db 4973 CGGCACTGGTCAACTTGGCCATGGTGCCCTCTCACGTGCTATTATTAAAGCAATTATC 4914
Qy 4103 TCGCTTGGTGGTCAATTCGAACCCAGAGTCCG----- 4137
Db 4913 AGGGTTATTGTCTCATGAGCGGATACATATTGAATGTATTAGAAAAATAACAATAG 4854
Qy 4138 ----- 4137
Db 4853 GGGTTCGGCGCACATTTCCCGAAAGTGCACCTGTATGCGGTGTGMAATACCGCACAG 4794
Qy 4138 -----CTCAGAAGAACTC 4150
Db 4793 ATCGTTAAGGAGAAAAATACCGCATCAGGAAATTTGAAGCGTTAATAATTACAGAAGACTC 4734
Qy 4151 GTCAAGAGCGGATAGAGCGATGCTCGGATCGGAGCGGCGGATACCGTTAAGAC 4210
Db 4733 GTCAAGAGCGGATAGAGCGATGCTCGGATCGGAGCGGCGGATACCGTTAAGAC 4674
Qy 4211 GAGGAAGCGGTAGCCCATTTCCGCGCAAGCTCTTCAGCAATATCACGGGTAGCCAAACG 4270
Db 4673 GAGGAAGCGGTAGCCCATTTCCGCGCAAGCTCTTCAGCAATATCACGGGTAGCCAAACG 4614
Qy 4271 TATGTCCTGATAGCGGTTCGCCACACCCAGCGCGGCCACAGTCGATGAATCCAGAAAGCG 4330
Db 4613 TATGTCCTGATAGCGGTTCGCCACACCCAGCGCGGCCACAGTCGATGAATCCAGAAAGCG 4554
Qy 4331 GCCATTTTCCACCATGATATTGGCAAGCAGGATCGCCATGGTCAACGAGATCCTC 4390
Db 4553 GCCATTTTCCACCATGATATTGGCAAGCAGGATCGCCATGGTCAACGAGATCCTC 4494
Qy 4391 GCCGTGGGATCGCGGCTTGAAGCTTGGCGAAGTTCGGCTGGCGGCGAGCCCTGATG 4450
Db 4493 GCCGTGGGATCGCGGCTTGAAGCTTGGCGAAGTTCGGCTGGCGGCGAGCCCTGATG 4434

Qy 4451 CTCCTTGTCCAGATCATCTCTGATCGAAGACCGGCTTCCATCCGAGTAGCTGCTCGTC 4510
Db 4433 CTCCTTGTCCAGATCATCTCTGATCGAAGACCGGCTTCCATCCGAGTAGCTGCTCGTC 4374
Qy 4511 GATCGAGTGTTCGCTTGGTGTGCAATGGGCGAGTAGCCGATCAAGCGTATGACGCG 4570
Db 4373 GATGCGATGTTCGCTTGGTGTGCAATGGGCGAGTAGCCGATCAAGCGTATGACGCG 4314
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Db 4313 CGCATTTGATCAGCATCATGATGATATCTTCTCGCAGGAGCAAGTGATGATGACAGGAG 4254
Qy 4631 ATCTGCCCCCGCATCTTGGCCCAATAGCAGCCAGTCCCTTCCGCTTCACTGACACGTC 4690
Db 4253 ATCTGCCCCCGCATCTTGGCCCAATAGCAGCCAGTCCCTTCCGCTTCACTGACACGTC 4194
Qy 4691 GAGCACAGCTGCGCAAGGAACGCCGTCGTGCGCAGCAGCATAGCCGCGCTGCTCCTC 4750
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Qy 4751 CTCGAGTTTCAATTCAGGGCACCGGACAGGTCTTGACAAAAAGAACCGGCGGCCCTG 4810
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Qy 4811 CGCTGACAGCCGGAACAACCGCGGCATCAGAGCAGCGATGCTGTGTGCGCCAGTCATA 4870
Db 4073 CGCTGACAGCCGGAACAACCGCGGCATCAGAGCAGCGATGCTGTGTGCGCCAGTCATA 4014
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Qy 5051 CGCCCCAGCTGGCAATTCGGGTTCGCTGTCTGTCATMAAACCGCCAGCTAGCTATCG 5110
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Qy 5171 GATAGCCAGTAGCTGACATTCATCCGGGTTCAGCACCGTTTCTGCGGACTGGCTTCTA 5230
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Qy 5231 CGTG 5234
Db 3653 CGTG 3650

Search completed: July 3, 2005, 07:52:29
Job time : 2975 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 3, 2005, 06:18:19 ; Search time 15530 Seconds
(without alignments)
12948.714 Million cell updates/sec

Title: US-09-921-143-36

Perfect score: 5283

Sequence: 1 agccttgaccttatgcgact.....tgagtgcttgcggcagcgtg 5283

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: gb_est1:*

2: gb_est2:*

3: gb_hic:*

4: gb_est3:*

5: gb_est4:*

6: gb_est5:*

7: gb_est6:*

8: gb_gss1:*

9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	991	18.8	2450	3 AK047844	AK047844 Mus muscu
2	948	17.9	1067	1 AU081137	AU081137 AU081137
3	939.4	17.8	954	7 CK283361	CK283361 EST746083
4	924.6	17.5	947	7 CK298208	CK298208 EST760922
5	919.8	17.4	1089	1 AU081124	AU081124 AU081124
6	918.6	17.4	935	7 CK284786	CK284786 EST740614
7	911	17.2	936	7 CK256977	CK256977 EST740614
8	907	17.2	910	7 CK287930	CK287930 EST750652
9	897.4	17.0	1049	9 CL021189	CL021189 CH216-8A1
10	886.4	16.8	933	7 CK291799	CK291799 EST754513
11	875	16.6	925	6 CB686151	CB686151 Bn01b 020
12	866.2	16.4	1073	7 CF269652	CF269652 FCYLC0148
13	859.2	16.3	885	9 CL076016	CL076016 CH216-138
14	843	16.0	856	7 CK287297	CK287297 EST750019
15	820.6	15.5	1025	9 CL021193	CL021193 CH216-8A1
16	818.6	15.5	1169	9 AG332951	AG332951 Mus muscu
17	809.2	15.3	966	8 BZ570738	BZ570738 msh2_1513
18	805.8	15.3	865	7 CK125894	CK125894 BBS182411
19	803	15.2	804	7 CK291519	CK291519 EST754233
20	794	15.0	811	7 CK288185	CK288185 EST750907
21	781.4	14.8	846	7 CV468077	CV468077 est_1_van
22	781.2	14.8	1163	1 AU081044	AU081044 AU081044
23	781.2	14.8	1249	8 BZ572284	BZ572284 msh2_2572
24	780.8	14.8	831	4 BG680919	BG680919 602628716

ALIGNMENTS

RESULT 1
AK047844
LOCUS
DEFINITION
Mus musculus 16 days embryo head cDNA, RIKEN full-length enriched library, clone: C130004M09 product: vascular endothelial growth factor C, full insert sequence.
ACCESSION
AK047844.1 GI:26339001
VERSION
AK047844.1
KEYWORDS
HTC; CAP trapper.
SOURCE
Mus musculus
ORGANISM
Mus musculus
REFERENCE
1 Carninci, P. and Hayashizaki, Y.
AUTHORS
Carninci, P. and Hayashizaki, Y.
TITLE
High-efficiency full-length cDNA cloning
JOURNAL
Meth. Enzymol. 303, 19-44 (1999)
MEDLINE
99279253
PUBMED
10349636
REFERENCE
2 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
AUTHORS
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
TITLE
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL
Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE
20499374
PUBMED
11042159
REFERENCE
3 Shinnoto, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, S., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
AUTHORS
Shinnoto, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, S., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
TITLE
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL
Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE
20530913
PUBMED
11076861
REFERENCE
4 The RIKEN Genome Exploration Research Group Phase II Team and the PANTOM Consortium.
AUTHORS
The RIKEN Genome Exploration Research Group Phase II Team and the PANTOM Consortium.
TITLE
Functional annotation of a full-length mouse cDNA collection
JOURNAL
Nature 409, 685-690 (2001)
MEDLINE
11076861
PUBMED
11076861
REFERENCE
5 The FANTOM Consortium and the RIKEN Genome Exploration Research

CA488579 AGENCOURT
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CR701632 Tetraodon
AZ687169 ENTMP05TF
BZ570648 msh2_1469

TITLE
JOURNAL
REFERENCE
AUTHORS

Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 2450)
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,
Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Haehizume, W.,
Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,
Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, T., Kasukawa, T.,
Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,
Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N.,
Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,
Sano, H., Sasaki, D., Shibata, K., Shingawa, A., Shiraki, T.,
Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,
Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
Muramatsu, M. and Hayashizaki, Y.

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COMMENT

CDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.
URL: <http://genome.gsc.riken.jp/>
Location/Qualifiers

FEATURES

source

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175. .1422

CDS

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ORIGIN

Query Match 18.8%; Score 991; DB 3; Length 2450;
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Matches 1121; Conservative 0; Mismatches 180; Indels 12; Gaps 1;
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QY 541 CTGCTCGCGCTCGCTCTCGGGGTCTCGAGGCGCCCGCGCGCCCGCTTC 600
Db 211 CTGCTCGCGCTCGCTGATCCCACTCCGAGCGAGGCGCCCGCCACCGCTCGCGCTTC 270

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RESULT 2
AU081137 1067 bp mRNA linear EST 30-JUL-2002
LOCUS AU081137 Oncorhynchus mykiss Kidney infected by infectious
DEFINITION hematopoietic necrosis virus Oncorhynchus mykiss cdna clone KI2,
mRNA sequence.
ACCESSION AU081137
VERSION AU081137.1 GI:6431485
KEYWORDS EST.
SOURCE Oncorhynchus mykiss (rainbow trout)
ORGANISM Oncorhynchus mykiss
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
REFERENCE 1 (bases 1 to 1067)
AUTHORS Kono,T., Sakai,M. and Lapetra,S.E.
TITLE Expressed Sequence Tag Analysis of Kidney and Gill Tissues from
Rainbow Trout (Oncorhynchus mykiss) Infected with Infectious
Hematopoietic Necrosis Virus
JOURNAL Mar. Biotechnol. 2 (5), 493-498 (2001)
COMMENT Contact: Masahiro Sakai
Faculty of Agriculture
Miyazaki University
1-1 nishi gakuenkibanadai, Miyazaki, Miyazaki 889-2192, Japan
Email: m.sakai@cc.miyazaki-u.ac.jp.
FEATURES
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RESULT 3

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DEFINITION EST746083 Nicotiana benthamiana mixed tissue cDNA library,
normalized, full-length Nicotiana benthamiana cDNA clone NEMAG50 5'
end, mRNA sequence.
ACCESSION CK283361
VERSION CK283361.1 GI:39855898
KEYWORDS EST.
SOURCE Nicotiana benthamiana
ORGANISM Nicotiana benthamiana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamiales; Solanales; Solanaceae; Nicotiana.
REFERENCE 1 (bases 1 to 954)
AUTHORS Buell,C.R., Hart,A., Zismann,V., Karamycheva,S.A., Day,B.,
Staakawicz,B., Jin,H. and Baker,B.
TITLE Generation of EST sequences from Nicotiana benthamiana
JOURNAL Unpublished (2003)
COMMENT Other ESTs: EST746084
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@tigr.org
Clones can be requested from the University of Arizona Genomics
Institute via http://genome.arizona.edu/orders/
Seq primer: ATT TAG GTG ACA CTA TAG.
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Matches 927; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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RESULT 5

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AU081124
LOCUS AU081124 1089 bp mRNA linear EST 30-JUL-2002
DEFINITION AU081124 Oncorhynchus mykiss Kidney infected by infectious
hematopoietic necrosis virus
mRNA sequence.
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ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

AU081124
AU081124.1 GI:6431472
EST.
Oncorhynchus mykiss (rainbow trout)

REFERENCE

1 (bases 1 to 1089)
Kono, T., Sakai, M. and Lapetra, S.E.
Expressed Sequence Tag Analysis of Kidney and Gill Tissues from
Rainbow Trout (Oncorhynchus mykiss) Infected with Infectious
Hematopoietic Necrosis Virus
Mar. Biotechnol. 2 (5), 493-498 (2001)

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

Location/Qualifiers

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ORIGIN

Query Match

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263 GCTGCATTAATGAATCGGCCAACGGCGGAGAGCGGCTTTCGCTATTTGGGCGCTCTTC 322

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443 GTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCGCGCTTCGTCGCGCTTTT 502

3126 CCATAGGCTTCGCGCCCTTCGAGAGATCCAAAAATCGACGCTCAAGTCAGAGGTGGCG 3185

503 CCATAGGCTTCGCGCCCTTCGAGAGATCCAAAAATCGACGCTCAAGTCAGAGGTGGCG 562

3186 AAACCCGACAGACTATTAAGATACCGCGCTTCCCTCGAGCTCCCTCGTCGCTC 3245

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3246 TCCTGTTCGACCCCTCGCGCTTACCGGATACCTGTCCGCTTCTCTCCCTTCGGAAGCGT 3305

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983 TCGGAAAAAGTGTGTAGTCTTTGGATCCGCAACAAACCAACCGCTGGGAAGGGGG 1042
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3661 GGTTTTTTTTGTGCAAGCA-GCAGATTACGCGCAGAAAAAAGGAT 3706
Qy
1043 TGTCTTTTGTGCAAGCAGCAGATTACCGCGGAAAAAAGCGAT 1089
Db

RESULT 6

CK284786/c
LOCUS
DEFINITION
EST747508 Nicotiana benthamiana mixed tissue cDNA library,
normalized, full-length Nicotiana benthamiana cDNA clone NBMAQ41 5'
end, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Nicotiana benthamiana
Nicotiana benthamiana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamiales; Solanales; Solanaceae; Nicotiana.
REFERENCE
1 (bases 1 to 935)
AUTHORS
Buell,C.R., Hart,A., Zismann,V., Karamycheva,S.A., Day,B.,
Staskawicz,B., Jin,H. and Baker,B.
The Institute for Genomic Research
Generation of EST sequences from Nicotiana benthamiana
Unpublished (2003)
Other ESTs: EST747509
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@igr.org
Clones can be requested from the University of Arizona Genomics
Institute via http://genome.arizona.edu/orders/
Seq primer: ATT TAG GTG ACA CTA TAG.

FEATURES

Source
1..935
/organism="Nicotiana benthamiana"
/mol_type="mRNA"
/db_xref="taxon:4100"
/clone="NBMAQ41"
/tissue_type="abiotic and biotic stress-treated leaves,
callus tissue and root tissue"
/lab_host="DH10B-TonA"
/clone_lib="Nicotiana benthamiana mixed tissue cDNA
library, normalized, full-length"
/notes="Vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI;
supplier: RNA was isolated from Nicotiana benthamiana
tissues that include callus, roots from liquid culture

grown plants, heat-stressed leaves (38 C, 3 hr and 6 hr),
cold-stressed leaves (5 C 3 hr, 6hr), and pathogen
challenged leaves (Pseudomonas syringae pv tomato 12 hr;
Xanthomonas campestris pv campestris 12 hr, 18hr;
Pseudomonas syringae pv phaseolicola 18hr, and Xanthomonas
campestris pv vesicatoria 18hr). RNA was isolated from
these tissues and pooled in approximately equal molar
amounts."

ORIGIN
Query Match 17.4%; Score 918.6; DB 7; Length 935;
Best Local Similarity 99.6%; Pred. No. 7.3e-253;
Matches 921; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 4030 AAAACGATTCGAAAGCCCAACCTTTTCATAGAAAGGCGCGGTGGAAATCGAAATCTCGTGAT 4089
Db 935 AAAACGATTCGAAAGCCCAACCTTTTCATAGAAAGGCGCGGTGGAAATCGAAATCTCGTGAT 876
QY 4090 GGCAGGTTGGGCGTCGCTTGGTCGGTCAATTTTCGAACCCCGAGAGTCCCGCTCAGAGAACT 4149
Db 875 GGCAGGTTGGGCGTCGCTTGGTCGGTCAATTTTCGAACCCCGAGAGTCCCGCTCAGAGAACT 816
QY 4150 CGTCAAGAGGCGATAGAAAGCGATCGCTCGGAATTCGGAACCCCGAGAGTCCCGCTCAGAGAACT 4209
Db 815 CGTCAAGAGGCGATAGAAAGCGATCGCTCGGAATTCGGAACCCCGAGAGTCCCGCTCAGAGAACT 756
QY 4210 CGAGAAAGGCTCAGCCCATTCGCGCCCAAGCTCTTCAGCAATATCAAGGATGACCAAG 4269
Db 755 CGAGAAAGGCTCAGCCCATTCGCGCCCAAGCTCTTCAGCAATATCAAGGATGACCAAG 696
QY 4270 CTATGCTCTGATAGCGGTCGCGCCACACCGCGGCGCAGTCGATGAATCCAGAAAAAGC 4329
Db 695 CTATGCTCTGATAGCGGTCGCGCCACACCGCGGCGCAGTCGATGAATCCAGAAAAAGC 636
QY 4330 GGCCTATTTTCCACCATGATATTCGGCAAGCAGGATTCGCCATGGGTTCAGACGAGATCCT 4389
Db 635 GGCCTATTTTCCACCATGATATTCGGCAAGCAGGATTCGCCATGGGTTCAGACGAGATCCT 576
QY 4390 CGCGCTGGGCGATGCGCGCTTTGAGCTGCGGCAAGCTTCGGCTGGCGGAGCCCTGAT 4449
Db 575 CGCGCTGGGCGATGCGCGCTTTGAGCTGCGGCAAGCTTCGGCTGGCGGAGCCCTGAT 516
QY 4450 GCTCTTTCGTCAGATCATCTGATCGAAGACCGGCTTCATCCGAGTACGTGCTCGCT 4509
Db 515 GCTCTTTCGTCAGATCATCTGATCGAAGACCGGCTTCATCCGAGTACGTGCTCGCT 456
QY 4510 CGATCGATGTTTCGCTTGGTGTGAAATGGGAGGTAGCCGGATCAAGCGTATGAGCC 4569
Db 455 CGATCGATGTTTCGCTTGGTGTGAAATGGGAGGTAGCCGGATCAAGCGTATGAGCC 396
QY 4570 GCGCATTTGCATCAGCCATGATGGATATCTTCTCGGAGGAGCAAGGTGAGATGACAGA 4629
Db 395 GCGCATTTGCATCAGCCATGATGGATATCTTCTCGGAGGAGCAAGGTGAGATGACAGA 336
QY 4630 GATCTGCCCCCGCACTTCGCCCAATAGCAGCAGTCCCTTCCCGCTTCAGTGACAACT 4689
Db 335 GATCTGCCCCCGCACTTCGCCCAATAGCAGCAGTCCCTTCCCGCTTCAGTGACAACT 276
QY 4690 CGAGCACAGCTCGCAAGAAACGCCCGTCGTGCGCCAGCCACGATAGCCCGCTGCTCGT 4749
Db 275 CGAGCACAGCTCGCAAGAAACGCCCGTCGTGCGCCAGCCACGATAGCCCGCTGCTCGT 216
QY 4750 CTTGAGTTCATTCAGGGCACCGGACAGGTTCGCTTGTGACAAAAGAAACCGGCGCCCT 4809
Db 215 CTTGAGTTCATTCAGGGCACCGGACAGGTTCGCTTGTGACAAAAGAAACCGGCGCCCT 156
QY 4810 GCGCTGACAGCCGGAACACCGCGCATCAGAGCAGCCGATTCGTGTTGTGCCAGTCAAT 4869
Db 155 GCGCTGACAGCCGGAACACCGCGCATCAGAGCAGCCGATTCGTGTTGTGCCAGTCAAT 96
QY 4870 AGCCGAATAGCTCTCCACCCCAAGCGCGGAGAACTCGCTGCAATCCATCTTGTTCAA 4929
Db 95 AGCCGAATAGCTCTCTCCACCCCAAGCGCGGAGAACTCGCTGCAATCCATCTTGTTCAA 36


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QY 4930 TCATCGGAAACGATCTCTCACTCTT 4954
Db 35 TCATCGGAAACGATCTCTCACTCTT 11

RESULT 7
CK256977/c
LOCUS EST740614 potato callus cDNA library, linear EST 30-JUL-2004
DEFINITION Solanum tuberosum cDNA clone POCD170 5' end, mRNA sequence.
ACCESSION CK256977
VERSION CK256977.1 GI:39813957
KEYWORDS EST.
SOURCE Solanum tuberosum (potato)
ORGANISM Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Solanum.
1 (bases 1 to 936)
Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A. and Baker, B.
Generation of ESTs from potato callus tissue
Unpublished (2003)
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@tigr.org
Clones can be requested from the University of Arizona Genomics
Institute via http://genome.arizona.edu/orders/
Seq primer: ATT TAG GTG ACA CTA TAG.

FEATURES
source
1..936
/organism="Solanum tuberosum"
/mol_type="mRNA"
/cultivar="Kennebec"
/db_xref="taxon:4113"
/clone="POCD170"
/tissue_type="callus"
/lab_host="DH108-Tona"
/clone_lib="potato callus cDNA library, normalized and
full-length"
/notes="Vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI;
supplier: RNA was isolated from Solanum tuberosum var.
Kennebec callus tissue grown on solid media."

ORIGIN
Query Match 17.2%; Score 911; DB 7; Length 936;
Best Local Similarity 99.9%; Pred. No. 1.1e-250;
Matches 922; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 4010 TCATCCAGCGCGGTCCC-GGAAACGATTCGGAAGCCCAACCTTTTCATAGAGCGCGG 4068
Db 936 TCATCCAGCGCGGTCCC-GGAAACGATTCGGAAGCCCAACCTTTTCATAGAGCGCGG 877

QY 4069 GTGGAATCGAAATCTCGTGTATGTCAGGTTGGGGGTGCGTTCGTCGTCATTTTCGAACCCC 4128
Db 876 GTGGAATCGAAATCTCGTGTATGTCAGGTTGGGGGTGCGTTCGTCGTCATTTTCGAACCCC 817

QY 4129 AGATGCCCGCTCAGAGAACTCGTCAAGAGGCGATAGAGGCGATCGCTCGCAATCGG 4188
Db 816 AGATGCCCGCTCAGAGAACTCGTCAAGAGGCGATAGAGGCGATCGCTCGCAATCGG 757

QY 4189 GAGCGGCGATACCGTAAAGCAGGAGCGGTTCAGCCCAATTCGCGCCCAAGCTTTCAG 4248
Db 756 GAGCGGCGATACCGTAAAGCAGGAGCGGTTCAGCCCAATTCGCGCCCAAGCTTTCAG 697

QY 4249 CAATATCAGCGGTAGCAACGCTATGTCCTGTATAGGTTCCGCGCACACCCAGCGGCCAC 4308
Db 696 CAATATCAGCGGTAGCAACGCTATGTCCTGTATAGGTTCCGCGCACACCCAGCGGCCAC 637

QY 4309 AGTCGATGAATCCAGAAAGCGGCCATTTTCCACCATGATATTTTCGGAAGCGGCATCGC 4368
Db 636 AGTCGATGAATCCAGAAAGCGGCCATTTTCCACCATGATATTTTCGGAAGCGGCATCGC 577
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QY 4369 CATGGGTACGACGAGATCTCGCGTCGGGCATATGCGCGCTTTCAGCTTCGCGAAACAGATT 4428
Db 576 CATGGGTACGACGAGATCTCGCGTCGGGCATATGCGCGCTTTCAGCTTCGCGAAACAGATT 517

QY 4429 CGSCTGGCGGAGCCCTGATGCTCTTCGTCAGATCATCTGATCGAACAAGACCGGCTT 4488
Db 516 CGSCTGGCGGAGCCCTGATGCTCTTCGTCAGATCATCTGATCGAACAAGACCGGCTT 457

QY 4489 CCATCCGAGTACGTCGTCGATCGATCGATGTTTCGCTGCTGTCGATCGAATGGCAGGTAG 4548
Db 456 CCATCCGAGTACGTCGTCGATCGATCGATGTTTCGCTGCTGTCGATCGAATGGCAGGTAG 397

QY 4549 CCGGATCAAGCGGTATGACGCGCGCATTCGATCAGCCATGATGGATACCTTCTCGGCAG 4608
Db 396 CCGGATCAAGCGGTATGACGCGCGCATTCGATCAGCCATGATGGATACCTTCTCGGCAG 337

QY 4609 GAGCAAGGTGAGATGACGAGAGATCTGCCCCGGGCACTTCGCCCAATAGCAGCAAGTCC 4668
Db 336 GAGCAAGGTGAGATGACGAGAGATCTGCCCCGGGCACTTCGCCCAATAGCAGCAAGTCC 277

QY 4669 TTCCCGCTTCAGTGACAAAGTCGAGCACAGCTGCGCAAGGAGCGCGCTCGTGGCGCAGCC 4728
Db 276 TTCCCGCTTCAGTGACAAAGTCGAGCACAGCTGCGCAAGGAGCGCGCTCGTGGCGCAGCC 217

QY 4729 AGCATAGCGCGCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4788
Db 216 AGCATAGCGCGCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 157

QY 4789 CAAAGAAACCGGGGCGCCCTCGCTGCTGACAGCGGAAACACGGCGGATCAGACAGCCGA 4848
Db 156 CAAAGAAACCGGGGCGCCCTCGCTGCTGACAGCGGAAACACGGCGGATCAGACAGCCGA 97

QY 4849 TTGTCGTTGTCGCCAGTATAGCCGATAGCTCTCCACCCAGCGCGGAGAACCTTG 4908
Db 96 TTGTCGTTGTCGCCAGTATAGCCGATAGCTCTCCACCCAGCGCGGAGAACCTTG 37

QY 4909 CGTGCAATCATCTTCTTCAATC 4931
Db 36 CGTGCAATCATCTTCTTCAATC 14

RESULT 8
CK287930/c
LOCUS 910 bp mRNA linear EST 02-AUG-2004
DEFINITION EST750652 Nicotiana benthamiana mixed tissue cDNA library,
normalized, full-length Nicotiana benthamiana cDNA clone NBMC75 5'
end, mRNA sequence.
ACCESSION CK287930
VERSION CK287930.1 GI:39864940
KEYWORDS EST.
SOURCE Nicotiana benthamiana
ORGANISM Nicotiana benthamiana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Nicotiana.
1 (bases 1 to 910)
Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A., Day, B.,
Staskiewicz, B., Jin, H. and Baker, B.
Generation of EST sequences from Nicotiana benthamiana
Unpublished (2003)
Other ESTs: EST750653
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@tigr.org
Clones can be requested from the University of Arizona Genomics
Institute via http://genome.arizona.edu/orders/
Seq primer: ATT TAG GTG ACA CTA TAG.

FEATURES
source
1..910
/organism="Nicotiana benthamiana"
/mol_type="mRNA"
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QY 2881 TGCAGCTGCTAATTAATGATCGCCCAACGCGCGGGAGAGCGGTTTGGCTATTTGGCGC 2940
Db 282 TGCAGCTGCTAATTAATGATCGCCCAACGCGCGGGAGAGCGGTTTGGCTATTTGGCGC 341
QY 2941 TCTTCGCTTCTCGCTCACTGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCT 3000
Db 342 TCTTCGCTTCTCGCTCACTGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCT 401
QY 3001 TCAGCTCACTCAAGAGCGGTAATACGGTTATCCACAGAAATCAGGGGATAACGACGAGGAAG 3060
Db 402 TCAGCTCACTCAAGAGCGGTAATACGGTTATCCACAGAAATCAGGGGATAACGACGAGGAAG 461
QY 3061 AACATGTGAGCAAAAGCGAGCAAAAGCGGACGAGAACCGTAAAGAGCGGTTGCTGGCG 3120
Db 462 AACATGTGAGCAAAAGCGAGCAAAAGCGGACGAGAACCGTAAAGAGCGGTTGCTGGCG 521
QY 3121 TTTTTCATAGGCTCCGCCCCCTGACGAGCATCACAAAATCAGACTCAAGTCAAGG 3180
Db 522 TTTTTCATAGGCTCCGCCCCCTGACGAGCATCACAAAATCAGACTCAAGTCAAGG 581
QY 3181 TGGCGAAACCGCAGCAGCACTATAAGATACAGGCGTTTCCCTCGGAAGCTCCCTCGTG 3240
Db 582 TGGCGAAACCGCAGCAGCACTATAAGATACAGGCGTTTCCCTCGGAAGCTCCCTCGTG 641
QY 3241 CGCTCTCTGTTCCGACCTGCGCTTACCGGATACCTGTCCGCTTTCTCCCTCGGGA 3300
Db 642 CGCTCTCTGTTCCGACCTGCGCTTACCGGATACCTGTCCGCTTTCTCCCTCGGGA 701
QY 3301 AGCGTGGCGCTTCTCATAGCTACGCTGTAGGTATCTCAGTTCCGTTGAGTGTGCTTCG 3360
Db 702 AGCGTGGCGCTTCTCATAGCTACGCTGTAGGTATCTCAGTTCCGTTGAGTGTGCTTCG 761
QY 3361 TCCAAGCTGGGCTGTGTGACAGAACCCCGTTTCCGCGGACCGCTGCGCTTATCCGCT 3420
Db 762 TCCAAGCTGGGCTGTGTGACAGAACCCCGTTTCCGCGGACCGCTGCGCTTATCCGCT 821
QY 3421 AACTATGCTTGTAGTCCAAACCGGTAAAGACACGACTTATCGCACTGGCAGAGCCACT 3480
Db 822 AACTATGCTTGTAGTCCAAACCGGTAAAGACACGACTTATCGCACTGGCAGAGCCACT 881
QY 3481 GGTAAACAGGATTAGCAGAGCGAGTATGATAGGCGGTGCTACAGAGTTCTTGAAGTGTG 3540
Db 882 GGTAAACAGGATTAGCAGAGCGAGTATGATAGGCGGTGCTACAGAGTTCTTGAAGTGTG 941
QY 3541 CCTAATCTACGGCTACACTAGAGAAC - AGTATTGTTGTTATCTGCTCTGCTGAGGCGAGT 3599
Db 942 CCTAATCTACGGCTACACTAGAGAACCAAGTATTGTTATCTGCGCTCTGCTGAAACCACT 1001
QY 3600 TACC-TTCGGAAGAGTTGGTAGCTCTTTGATCCGCGCAACAAACC 3645
Db 1002 TACCTTTCGGAAGAGTTGGTAGCTCTTTGATCCGCGCAACAAACC 1048

RESULT 10
CK291799/c

LOCUS
DEFINITION
CK291799.1 933 bp mRNA linear EST 02-AUG-2004
EST754513 Nicotiana benthamiana mixed tissue cDNA library
normalized, full-length Nicotiana benthamiana cDNA clone NEMC477 5'
end, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE

CK291799
CK291799.1 GI:39872608
EST.
Nicotiana benthamiana
Nicotiana benthamiana
Nicotiana benthamiana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamiales; Solanales; Solanaceae; Nicotiana.

REFERENCE
AUTHORS

1 (bases 1 to 933)
Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A., Day, B.,
Straskawicz, B., Jin, H. and Baker, B.
Generation of EST sequences from Nicotiana benthamiana
Unpublished (2003)
Other ESTs: EST754514

FEATURES
source

1..933
/organism="Nicotiana benthamiana"
/mol_type="mRNA"
/db_xref="taxon:4100"
/clone="NEMC477"
/tissue_type="abiotic and biotic stress-treated leaves,
callus tissue and root tissue"
/lab_host="DH10B-Tona"
/clone_lib="Nicotiana benthamiana mixed tissue cDNA
library, normalized, full-length"
/notes="Vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI;
supplier: RNA was isolated from Nicotiana benthamiana
tissues that include callus, roots from liquid culture
grown plants, heat-stressed leaves (38 C, 3 hr and 6 hr),
cold-stressed leaves (5 C 3 hr, 6hr), and pathogen
challenged leaves (Pseudomonas syringae pv tomato 12 hr;
Xanthomonas campestris pv campestris 12 hr, 18hr;
Pseudomonas syringae pv phaseolicola 18hr, and Xanthomonas
campestris pv vesicatoria 18hr). RNA was isolated from
these tissues and pooled in approximately equal molar
amounts."

ORIGIN

Query Match 16.8%; Score 886.4; DB 7; Length 933;
Best Local Similarity 99.9%; Pred. No. 1.4e-243;
Matches 887; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 4044 GCCCAACCTTTTCATAGAAGCGCGCTGGAATCGAAATCTCGTATGGCAGGTTGGCGCT 4103
Db 933 GCCCAACCTTTTCATAGAAGCGCGCTGGAATCGAAATCTCGTATGGCAGGTTGGCGCT 874
QY 4104 CGCTTGGTGGCTCATTTTCGAAACCCAGAGTCCCGCTCAGAGAACTCGTCAAGAGCGCA 4163
Db 873 CGCTTGGTGGCTCATTTTCGAAACCCAGAGTCCCGCTCAGAGAACTCGTCAAGAGCGCA 814
QY 4164 TAGAAGCGGATGGCTGCGAATCGGAGCGGCGATACCGTAAAGACGAGAGAGCGTCA 4223
Db 813 TAGAAGCGGATGGCTGCGAATCGGAGCGGCGATACCGTAAAGACGAGAGAGCGTCA 754
QY 4224 GCCCATTCGCGCAAGCTCTTCAGCAATATACGCGGTAGCCAAACGCTATGTCTCTGATAG 4283
Db 753 GCCCATTCGCGCAAGCTCTTCAGCAATATACGCGGTAGCCAAACGCTATGTCTCTGATAG 694
QY 4284 CGGTCCGCGACACCCAGCGGCGACAGTCAATTCAGAAAGAGGCGGCATTTTCACAC 4343
Db 693 CGGTCCGCGACACCCAGCGGCGACAGTCAATTCAGAAAGAGGCGGCATTTTCACAC 634
QY 4344 ATGATATTCGGAAGCAGGATCGCCATCGCTCAGCAGAGATCCCTCGCGTGGGCATG 4403
Db 633 ATGATATTCGGAAGCAGGATCGCCATCGCTCAGCAGAGATCCCTCGCGTGGGCATG 574
QY 4404 CGCGCTTGGAGCTTGGCGAACAGTTCGCTGGCGGAGGCCCTCTGATGCTCTTCTGTCAGA 4463
Db 573 CGCGCTTGGAGCTTGGCGAACAGTTCGCTGGCGGAGGCCCTCTGATGCTCTTCTGTCAGA 514
QY 4464 TCATCTGTATGCAAGACCGGCTTCATTCGAGTACGCTGCTCGTTCGATGCGATGTTTC 4523
Db 513 TCATCTGTATGCAAGACCGGCTTCATTCGAGTACGCTGCTCGTTCGATGCGATGTTTC 454
QY 4524 GCTTGTGTGCGAATGGGCGAGGTAGCCGATCAAGCGTATGAGCCGCGCATTTGCATCA 4583
Db 453 GCTTGTGTGCGAATGGGCGAGGTAGCCGATCAAGCGTATGAGCCGCGCATTTGCATCA 394
QY 4584 GCCATGATGATCTTTCTTCGCGAGGAGCAAGGTGAGATGACAGGAGATCTCTGCCCGCGC 4643

Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@tigr.org
Clones can be requested from the University of Arizona Genomics
Institute via http://genome.arizona.edu/orders/
Seq primer: ATT TAG GTG ACA CTA TAG.

Location/Qualifiers

Db 393 GCCATGATGATACTTTCTCGGAGGAGCAAGGTGAGATGACAGGAGATCTCTGCCCGGC 334
QY 4644 ACTTCGCCCAATAGAGCCAGTCCCTTCGGCTTCAGTACAACTCGAGCAGCTGG 4703
Db 333 ACTTCGCCCAATAGAGCCAGTCCCTTCGGCTTCAGTACAACTCGAGCAGCTGG 274
QY 4704 CAAGGAACGCCGCTCGTGGCCAGCCACGATAGCCGGCTGCCTCGTTCCTGCAAGTTCATTC 4763
Db 273 CAAGGAACGCCGCTCGTGGCCAGCCACGATAGCCGGCTGCCTCGTTCCTGCAAGTTCATTC 214
QY 4764 AGGCAACGCCGCTCGTGGCCAGCCACGATAGCCGGCTGCCTCGTTCCTGCAAGTTCATTC 4823
Db 213 AGGCAACGCCGCTCGTGGCCAGCCACGATAGCCGGCTGCCTCGTTCCTGCAAGTTCATTC 154
QY 4824 AACACGGCGGCATCAGAGCAGCGGATTCCTGTTGGCCAGTCATAGCCGATAGCCTC 4883
Db 153 AACACGGCGGCATCAGAGCAGCGGATTCCTGTTGGCCAGTCATAGCCGATAGCCTC 94
QY 4884 TCCACCACGCGCCGAGAACCTCGTGCATTCATTCATTCATTC 4931
Db 93 TCCACCACGCGCCGAGAACCTCGTGCATTCATTCATTCATTC 46

RESULT 11

CB686151/c

LOCUS

DEFINITION

Bn01b_02o08 A 925 bp mRNA linear EST 09-APR-2003
Bn01b_AAPC_ECORC_transgenic_Brassica_napus_overexpressing_BNCB17_c
onstitutively_frost_tolerant Brassica napus cDNA clone Bn01b_02o08,
mRNA sequence.

ACCESSION

CB686151

VERSION

CB686151.1

KEYWORDS

EST.

SOURCE

Brassica napus (rape)

ORGANISM

Brassica napus

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

1. (bases 1 to 925)

Singh, J., Allard, G., Tinker, N., Robert, L., Lacroix, C., De Moors, A.,

Chagnon, J., Farah, S., Couroux, P., and Hattori, J.

Expressed Sequence Tags from constitutively frost tolerant

transgenic Brassica napus overexpressing BNCB17

Unpublished (2002)

Contact: Singh, J.A.

Eastern Cereal and Oilseed Research Centre

Agriculture and Agri-food Canada

KW Neatby Bldg., Central Experimental Farm, Ottawa, Ontario, K1A

OC6, Canada

Tel: (613) 759-1662

Fax: (613) 759-1701

Email: singhja@agr.gc.ca.

Location/Qualifiers

1. .925

/organism="Brassica napus"

/mol_type="mRNA"

/cultivar="Westar"

/db_xref="taxon:3708"

/clone="Bn01b_02o08"

/issue_type="fourth leaf"

/dev_stage="3 weeks seedling grown at room temperature"

/clone_lib="Bn01b_AAPC_ECORC_transgenic_Brassica_napus_ove

rpressing_BNCB17_constitutively_frost_tolerant"

/notes="Vector: Bluescript SK+/XhoI-EcoRI; Site 1: EcoRI;

Site 2: XhoI; Germinated in soil flats and seedlings grown

for 3 weeks in a Conviron E-15 cabinet set at 20oC /16 hr

light (250 Em-2sec-1) and 16 oC / 8 hr dark. Fourth leaves

collected at 9 am and immediately frozen."

Query Match

Best Local Similarity 16.6%; Score 875; DB 6; Length 925;

Matches 886; Conservative 6; Mismatches 6; Indels 1; Gaps 1;

QY 2701 GCTGTAGAGTAAATCATGTTCATAGCTGTTTCTCTGTGTAATGTTATCCGCTCACA 2760
Db 898 GGGCGCTTGGCGTAATCATGTTCATAGCTGTTT - CTGTGTAATGTTATCCGCTCACA 840
QY 2761 ATTTCACACAAATACGAGCCGGAAGTGTAAAGCTTGGGGTGCCTTAATGAGTG 2820
Db 839 ATTTCACACAAATACGAGCCGGAAGTGTAAAGCTTGGGGTGCCTTAATGAGTG 780
QY 2821 AGCTAACTCAATTAATTTGGTTCAGTCCCGCTTTCCAGTTCGGGAACTGTGCG 2880
Db 779 AGCTAACTCAATTAATTTGGTTCAGTCCCGCTTTCCAGTTCGGGAACTGTGCG 720
QY 2881 TGCCAGCTGCAATTAATGAATCGGCCAAGCGCGGGAGAGCGGTTTCGCTATTTCGGGCG 2940
Db 719 TGCCAGCTGCAATTAATGAATCGGCCAAGCGCGGGAGAGCGGTTTCGCTATTTCGGGCG 660
QY 2941 TCTTCGGCTTCCTCGCTCACTGACTCGCTCGGCTCGGTCGTTTCGGCTCGGCGAGCGGTA 3000
Db 659 TCTTCGGCTTCCTCGCTCACTGACTCGCTCGGCTCGGTCGTTTCGGCTCGGCGAGCGGTA 600
QY 3001 TCAGCTCACTCAAGGCGGTAATACGGTTATCCACAGAAATCAGGGGATAACGACAGAAAG 3060
Db 599 TCAGCTCACTCAAGGCGGTAATACGGTTATCCACAGAAATCAGGGGATAACGACAGAAAG 540
QY 3061 AACATGTGAGCAAAAGGCGCAGCAAGGCGCAGGAAACCGTAAAGAGGCGCGTTGCTGGCG 3120
Db 539 AACATGTGAGCAAAAGGCGCAGCAAGGCGCAGGAAACCGTAAAGAGGCGCGTTGCTGGCG 480
QY 3121 TTTTTCCTATAGCTCGCGCCCTCGCTGACGAGCATCAAAAAATCGACGCTCAAGTCAGAGG 3180
Db 479 TTTTTCCTATAGCTCGCGCCCTCGCTGACGAGCATCAAAAAATCGACGCTCAAGTCAGAGG 420
QY 3181 TGGCGAAACCCGACAGGACTATAAGATAACGGGCTTTCCCTCTGGAAGCTCCCTCGTG 3240
Db 419 TGGCGAAACCCGACAGGACTATAAGATAACGGGCTTTCCCTCTGGAAGCTCCCTCGTG 360
QY 3241 CGCTCTCTGTTCCGACCTCGCTTACCGATACCTGTCGCGCTTTCTCCCTTCGCGA 3300
Db 359 CGCTCTCTGTTCCGACCTCGCTTACCGATACCTGTCGCGCTTTCTCCCTTCGCGA 300
QY 3301 AGCGTGGCGCTTTCTCATAGCTCACTGATAGTATCTCAGTTCGGTGTAGTTCGCTCGC 3360
Db 299 AGCGTGGCGCTTTCTCATAGCTCACTGATAGTATCTCAGTTCGGTGTAGTTCGCTCGC 240
QY 3361 TCCAAAGCTGGGCTGTGTGCAAGAACCCCGCTTACGCCGAGCGCTGCGCTTATCCGCT 3420
Db 239 TCCAAAGCTGGGCTGTGTGCAAGAACCCCGCTTACGCCGAGCGCTGCGCTTATCCGCT 180
QY 3421 AACTATCGTCTTGTAGTCCAAACCGGTAAAGACACGACTTATCGCCACTGCGACGCACT 3480
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QY 3481 GGTAACAGGATTAGCAGAGCGAGGTATGTAGCGGTGTCTACAGAGTCTTCTGAAGTGGTG 3540
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RESULT 12

CF269652

LOCUS

DEFINITION

CF269652 1073 bp mRNA linear EST 13-AUG-2003
Fcylcoid844 Fragilariopsis cylindrus SMART cDNA library (Clontech)

Fragilariopsis cylindrus cDNA clone Antarctic 5', mRNA sequence.

ACCESSION

CF269652

VERSION

CF269652.1

KEYWORDS

EST.

SOURCE

Fragilariopsis cylindrus

Fragilariopsis cylindrus

ORGANISM

Eukaryota; stramenopiles; Bacillariophyta; Bacillariophyceae;

REFERENCE AUTHORS TITLE	JOURNAL COMMENT
Bacillariophycidae; Bacillariales; Bacillariaceae; Fragilariopsis. 1 (bases 1 to 1073) Mock,T. and Valentin,K. EST analysis of freezing tolerance in the Antarctic diatom Fragilariopsis cylindrus: Detection of numerous cold adaptation related genes and gene transfer events Unpublished (2003) Contact: Mock T Biological Oceanography Alfred-Wegener-Institute for Polar and Marine Research Am Handelshafen 12, D-27570 Bremerhaven, Germany Tel.: +49 471 4831 1893 Fax: +49 471 4831 1425 Email: tmock@awi-bremerhaven.de PCR Primers FORWARD: 5'lambdaTriplex2 BACKWARD: 3'lambdaTriplex2 Seq primer: ctggggaagcgccattgtgttgggt. Location/Qualifiers 1..1073 /organism="Fragilariopsis cylindrus" /mol_type="mRNA" /strain="Antarctic" /db_xref="taxon:186039" /clone_lib="Fragilariopsis cylindrus SMART cDNA library (Clontech)" /notes="Vector: pTriplex2; total polyA was used for first-strand synthesis with SMART IV oligos and CDS 111/3 PCR primer. Double strand cDNA synthesis was done by LD PCR using the following program: 95oC for 5 min denaturation and subsequent 20 cycles at 95oC (2min) and 68oC (6min). After SfiI digestion the cDNA was fractionated with CHROMA Spin-400 columns. These cDNAs were ligated overnight into pTriplex2 vectors." <td></td>	
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DB 61 ATCGGCCAACGCGGGGAGAGCGGTTTCGGTATTTGGGCGCTTTCGCTTCTCGCTC 120 	
QY 2959 ACTGACTCGCTCGGCTCGGTCTGGCTCGGCGAGCGGTATCAGCTCACTCAAAGCG 3018 	
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DB 361 CTATAAGATACAGGCGTTTCCGCCCTTGGAGGCTCCCTCGTGGGCTCTCCTGTTCCGACC 420 	
QY 3259 CTGCGGTTACCGGATACCTGTGCGCCTTCTCCCTTCGGGAACGCGTTCCTTCAT 3318 	
DB 421 CTGCGGTTACCGGATACCTGTGCGCCTTCTCCCTTCGGGAACGCGTTCCTTCAT 480 	


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RESULT 15
LOCUS CL021193
DEFINITION CH216-8A16.RM1.1 CH216 Xenopus tropicalis genomic clone CH216-8A16,
genomic survey sequence.
ACCESSION CL021193
VERSION CL021193.1 GI:40463006
KEYWORDS GSS.
SOURCE Xenopus tropicalis (western clawed frog)
ORGANISM Xenopus tropicalis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
Xenopodinae; Xenopus; Silurana.
REFERENCE 1 (bases 1 to 1025)
AUTHORS Kremitzki, C., Carter, J., McPherson, J., Warren, W., Graves, T.,
Mardis, E., and Wilson, R.
TITLE A physical map of the xenopus tropicalis genome
JOURNAL Unpublished (2003)
COMMENT Contact: Richard K Wilson
Genome Sequencing Center
Washington University School of Medicine
Email: submissions@wustl.edu
Insert Length: 175000 Std Error: 0.00
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FEATURES
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ORIGIN

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BAC library"
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